

-6-

Ala	Leu	Val	Gln	Leu	Cys	Gly	Thr	Tyr	Pro	Pro	Ser	Tyr	Asn	Leu	Thr
	290					295					300				
Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr
305					310					315					320
Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg
				325					330					335	
Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn
			340					345					350		
Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp
	355						360					365			
Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	Lys	Val	Ser	Phe	Lys	Phe
	370					375					380				
Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp
385					390					395					400
Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe
				405					410					415	
Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp
			420					425					430		
Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp
	435						440					445			
Ser	Ser	Asp	Pro	Cys	Pro	Gly	Gln	Phe	Thr	Cys	Arg	Thr	Gly	Arg	Cys
	450					455					460				
Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His
465					470					475					480
Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys
				485					490					495	
Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Val	Asn
			500					505					510		
Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Ser	Cys	Pro	Ala	Gln
	515					520						525			
Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Ser	Lys	Ser	Gln	Gln	Cys
	530					535					540				
Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Ala	Ser	Cys	Pro
545					550					555					560
Lys	Val	Asn	Val	Val	Thr	Cys	Thr	Lys	His	Thr	Tyr	Arg	Cys	Leu	Asn
				565					570					575	
Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	Glu	Cys	Asp	Gly	Lys	Glu	Asp
			580					585						590	
Cys	Ser	Asp	Gly	Ser	Asp	Glu	Lys	Asp	Cys	Asp	Cys	Gly	Leu	Arg	Ser
	595					600						605			
Phe	Thr	Arg	Gln	Ala	Arg	Val	Val	Gly	Gly	Thr	Asp	Ala	Asp	Glu	Gly
	610					615					620				
Glu	Trp	Pro	Trp	Gln	Val	Ser	Leu	His	Ala	Leu	Gly	Gln	Gly	His	Ile
625					630					635					640
Cys	Gly	Ala	Ser	Leu	Ile	Ser	Pro	Asn	Trp	Leu	Val	Ser	Ala	Ala	His
				645					650					655	
Cys	Tyr	Ile	Asp	Asp	Arg	Gly	Phe	Arg	Tyr	Ser	Asp	Pro	Thr	Gln	Trp
			660					665					670		
Thr	Ala	Phe	Leu	Gly	Leu	His	Asp	Gln	Ser	Gln	Arg	Ser	Ala	Pro	Gly
	675						680					685			
Val	Gln	Glu	Arg	Arg	Leu	Lys	Arg	Ile	Ile	Ser	His	Pro	Phe	Phe	Asn
	690					695					700				
Asp	Phe	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Glu	Lys	Pro
705					710					715					720
Ala	Glu	Tyr	Ser	Ser	Met	Val	Arg	Pro	Ile	Cys	Leu	Pro	Asp	Ala	Ser
				725					730					735	
His	Val	Phe	Pro	Ala	Gly	Lys	Ala	Ile	Trp	Val	Thr	Gly	Trp	Gly	His
			740					745					750		
Thr	Gln	Tyr	Gly	Gly	Thr	Gly	Ala	Leu	Ile	Leu	Gln	Lys	Gly	Glu	Ile
	755						760					765			

-7-

Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
 770 775 780
 Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
 785 790 795 800
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
 805 810 815
 Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
 820 825 830
 Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
 835 840 845
 Ile Lys Glu Asn Thr Gly Val
 850 855

<210> 3
 <211> 2137
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (261)...(1574)
 <223> Nucleic acid encoding a transmembrane serine
 protease (MTSP3) protein

<400> 3
 ccatacctaatacgcactcactatagggctcagcggccgcccgggcagggtcagagagagggc 60
 agcagcttgctcagcgggacaggatgctggcggtgaggggacaaaggcctgccctgcactc 120
 gggcctcctccagccagtgcagccagggaattctgacctgctggccagccaggacctgt 180
 gtggggaggccctcctgctgccttgggggtgacaatctcagctccaggctaaggagagacc 240
 gggaggatcacagagccagc atg tta cag gat cct gac agt gat caa cct ctg 293
 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu
 1 5 10
 aac agc ctc gat gtc aaa ccc ctg cgc aaa ccc cgt atc ccc atg gag 341
 Asn Ser Leu Asp Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu
 15 20 25
 acc ttc aga aag gtg ggg atc ccc atc atc ata gca cta ctg agc ctg 389
 Thr Phe Arg Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu
 30 35 40
 gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa 437
 Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys
 45 50 55
 tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag 485
 Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 60 65 70 75
 ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac 533
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His
 80 85 90
 tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc 581
 Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser
 95 100 105
 aag gac cga tcc aca ctg cag gtg ctg gac tcg gcc aca ggg aac tgg 629
 Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp
 110 115 120

-8-

ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala 125 130 135	677
tgt agg cag atg ggc tac agc agc aaa ccc acc ttc aga gct gtg gag Cys Arg Gln Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu 140 145 150 155	725
att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser 160 165 170	773
cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser 175 180 185	821
ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro 190 195 200	869
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln 205 210 215	917
gtc agc atc cag tac gac ata cag cac gtc tgt gga ggg agc atc ctg Val Ser Ile Gln Tyr Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu 220 225 230 235	965
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr 240 245 250	1013
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser 255 260 265	1061
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro 270 275 280	1109
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro 285 290 295	1157
ctc act ttc tca ggc aca gtc agg ctc atc tgt ctg ccc ttc ttt gat Leu Thr Phe Ser Gly Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp 300 305 310 315	1205
gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe 320 325 330	1253
acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser 335 340 345	1301
gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln 350 355 360	1349
ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt	1397

-9-

Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly
 365 370 375
 gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct 1445
 Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser 395
 380 385
 gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg 1493
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly 410
 400 405
 ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac 1541
 Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn 425
 415 420
 tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgctgcc cctttgcagt 1594
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu * 435
 430
 gctgggagcc gcttccttcc tgcctgccc acctggggat cccccaaagt cagacacaga 1654
 gcaagagtcc ccttgggtac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1714
 agggcctcaa ttcctgtaag agaccctcgc agcccagagg cgcccagagg aagtcagcag 1774
 ccctagctcg gccacacttg gtgctcccag catcccaggg agagacacag cccactgaac 1834
 aaggtctcag ggggtattgct aagccaagaa ggaactttcc cacactactg aatggaagca 1894
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa gggctctgcgc 1954
 cagccctgtc cgtcttcacc catccccaag cctactagag caagaaacca gttgtaatat 2014
 aaaatgcact gccctactgt tggatatgact accgttacct actgttgtca ttgttattac 2074
 agctatggcc actattatta aagagctgtg taacaaaaaa aaaaaaaaaa aaaaaaaaaa 2134
 aaa 2137
 <210> 4
 <211> 437
 <212> PRT
 <213> Homo Sapien
 <400> 4
 Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1 5 10 15
 Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
 20 25 30
 Gly Ile Pro Ile Ile Ile Ala Leu Ser Leu Ala Ser Ile Ile Ile
 35 40 45
 Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
 50 55 60
 Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
 65 70 75 80
 Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
 85 90 95
 Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
 100 105 110
 Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
 115 120 125
 Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly
 130 135 140
 Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
 145 150 155 160
 Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
 165 170 175
 Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
 180 185 190
 Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly

-10-

```

      195      200      205
Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
  210      215      220
Asp Ile Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
  225      230      235      240
Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
      245      250      255
Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
      260      265      270
Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
      275      280      285
Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
      290      295      300
Thr Val Arg Leu Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
  305      310      315      320
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
      325      330      335
Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
      340      345      350
Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
      355      360      365
Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
      370      375      380
Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
  385      390      395      400
Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
      405      410      415
Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val
      420      425      430
Trp Lys Ala Glu Leu
      435

```

<210> 5
 <211> 708
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1)...(708)
 <223> Nucleic acid encoding an MTSP4 protease domain

```

<400> 5
att gtt ggt gga gct gtg tcc tcc gag ggt gag tgg cca tgg cag gcc      48
ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala
  1          5          10          15

agc ctc cag gtt cgg ggt cga cac atc tgt ggg ggg gcc ctc atc gct      96
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
      20          25          30

gac cgc tgg gtg ata aca gct gcc cac tgc ttc cag gag gac agc atg      144
Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
      35          40          45

gcc tcc acg gtg ctg tgg acc gtg ttc ctg ggc aag gtg tgg cag aac      192
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
      50          55          60

tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg      240
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu

```

-11-

65	70	75	80	
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg				288
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu	85	90	95	
cag ctc gac cac ccg gtg gtg cgc tgc gcc gcc gtg cgc ccc gtc tgc				336
Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys	100	105	110	
ctg ccc gcg cgc tcc cac ttc ttc gag ccc ggc ctg cac tgc tgg att				384
Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile	115	120	125	
acg ggc tgg ggc gcc ttg cgc gag ggc ggc ccc atc agc aac gct ctg				432
Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu	130	135	140	
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc				480
Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val	145	150	155	160
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc ggc tac cgc aag				528
Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys	165	170	175	
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc				576
Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys	180	185	190	
aag gca ctc agt ggc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg ggc				624
Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly	195	200	205	
ctg ggc tgt ggc cgc cct aac tac ttc ggc gtc tac acc cgc atc aca				672
Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr	210	215	220	
ggc gtg atc agc tgg atc cag caa gtg gtg acc tga				708
Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *	225	230	235	

<210> 6
 <211> 235
 <212> PRT
 <213> Homo Sapien

<400> 6
 Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala
 1 5 10 15
 Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
 20 25 30
 Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
 35 40 45
 Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
 50 55 60
 Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu
 65 70 75 80
 His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
 85 90 95

-12-

Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
 100 105 110
 Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
 115 120 125
 Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
 130 135 140
 Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
 145 150 155 160
 Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
 165 170 175
 Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 180 185 190
 Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
 195 200 205
 Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
 210 215 220
 Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr
 225 230 235

<210> 7
 <211> 3104
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (33)...(2441)
 <223> Nucleic acid encoding MTSP4-L (long form) splice variant

<400> 7
 tcacgcggcca gaggggtgatc agtgagcaga ag atg ccc gtg gcc gag gcc ccc 53
 Met Pro Val Ala Glu Ala Pro
 1 5
 cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag 101
 Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu
 10 15 20
 ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg 149
 Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg
 25 30 35
 ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg 197
 Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val
 40 45 50 55
 ctg gct tcg gcg ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg 245
 Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala
 60 65 70
 gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat 293
 Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn
 75 80 85
 cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc 341
 Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg
 90 95 100
 agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc 389
 Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser
 105 110 115

-13-

acc	cgc	ctg	gga	act	tac	tac	aac	tcc	agc	tcc	gtc	tat	tcc	ttt	ggg	437
Thr	Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	
120					125					130					135	
gag	gga	ccc	ctc	acc	tgc	ttc	ttc	tgg	ttc	att	ctc	caa	atc	ccc	gag	485
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	Glu	
				140					145					150		
cac	cgc	cgg	ctg	atg	ctg	agc	ccc	gag	gtg	gtg	cag	gca	ctg	ctg	gtg	533
His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	Leu	Val	
			155					160					165			
gag	gag	ctg	ctg	tcc	aca	gtc	aac	agc	tgc	gct	gcc	gtc	ccc	tac	agg	581
Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	Pro	Tyr	Arg	
		170					175					180				
gcc	gag	tac	gaa	gtg	gac	ccc	gag	ggc	cta	gtg	atc	ctg	gaa	gcc	agt	629
Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	Leu	Glu	Ala	Ser	
	185					190					195					
gtg	aaa	gac	ata	gct	gca	ttg	aat	tcc	acg	ctg	ggc	tgt	tac	cgc	tac	677
Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	Gly	Cys	Tyr	Arg	Tyr	
200					205					210					215	
agc	tac	gtg	ggc	cag	ggc	cag	gtc	ctc	cgg	ctg	aag	ggg	cct	gac	cac	725
Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	Leu	Lys	Gly	Pro	Asp	His	
				220					225					230		
ctg	gcc	tcc	agc	tgc	ctg	tgg	cac	ctg	cag	ggc	ccc	aag	gac	ctc	atg	773
Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	Gln	Gly	Pro	Lys	Asp	Leu	Met	
			235				240					245				
ctc	aaa	ctc	cgg	ctg	gag	tgg	acg	ctg	gca	gag	tgc	cgg	gac	cga	ctg	821
Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	
		250					255					260				
gcc	atg	tat	gac	gtg	gcc	ggg	ccc	ctg	gag	aag	agg	ctc	atc	acc	tgc	869
Ala	Met	Tyr	Asp	Val	Ala	Gly	Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	
	265					270					275					
gtg	tac	ggc	tgc	agc	cgc	cag	gag	ccc	gtg	gtg	gag	gtt	ctg	gcg	tgc	917
Val	Tyr	Gly	Cys	Ser	Arg	Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	
280					285				290						295	
ggg	gcc	atc	atg	gcg	gtc	gtc	tgg	aag	aag	ggc	ctg	cac	agc	tac	tac	965
Gly	Ala	Ile	Met	Ala	Val	Val	Trp	Lys	Lys	Gly	Leu	His	Ser	Tyr	Tyr	
				300					305					310		
gac	ccc	ttc	gtg	ctc	tcc	gtg	cag	ccg	gtg	gtc	ttc	cag	gcc	tgt	gaa	1013
Asp	Pro	Phe	Val	Leu	Ser	Val	Gln	Pro	Val	Val	Phe	Gln	Ala	Cys	Glu	
			315					320					325			
gtg	aac	ctg	acg	ctg	gac	aac	agg	ctc	gac	tcc	cag	ggc	gtc	ctc	agc	1061
Val	Asn	Leu	Thr	Leu	Asp	Asn	Arg	Leu	Asp	Ser	Gln	Gly	Val	Leu	Ser	
		330					335					340				
acc	ccg	tac	ttc	ccc	agc	tac	tac	tgc	ccc	caa	acc	cac	tgc	tcc	tgg	1109
Thr	Pro	Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser	Pro	Gln	Thr	His	Cys	Ser	Trp	
	345					350					355					

-14-

cac His 360	ctc Leu	acg Thr	gtg Val	ccc Pro	tct Ser 365	ctg Leu	gac Asp	tac Tyr	ggc Gly 370	ttg Leu	gcc Ala	ctc Leu	tgg Trp	ttt Phe	gat Asp 375	1157
gcc Ala	tat Tyr	gca Ala	ctg Leu	agg Arg 380	agg Arg	cag Gln	aag Lys	tat Tyr	gat Asp 385	ttg Leu	ccg Pro	tgc Cys	acc Thr	cag Gln 390	ggc Gly	1205
cag Gln	tgg Trp	acg Thr	atc Ile 395	cag Gln	aac Asn	agg Arg	agg Arg	ctg Leu 400	tgt Cys	ggc Gly	ttg Leu	cgc Arg	atc Ile 405	ctg Leu	cag Gln	1253
ccc Pro	tac Tyr	gcc Ala 410	gag Glu	agg Arg	atc Ile	ccc Pro	gtg Val 415	gtg Val	gcc Ala	acg Thr	gcc Ala	ggg Gly 420	atc Ile	acc Thr	atc Ile	1301
aac Asn 425	ttc Phe	acc Thr	tcc Ser	cag Gln	atc Ile	tcc Ser 430	ctc Leu	acc Thr	ggg Gly	ccc Pro	ggt Gly 435	gtg Val	cgg Arg	gtg Val	cac His	1349
tat Tyr 440	ggc Gly	ttg Leu	tac Tyr	aac Asn	cag Gln	tcg Ser 445	gac Asp	ccc Pro	tgc Cys	cct Pro	gga Gly	gag Glu	ttc Phe	ctc Leu	tgt Cys 455	1397
tct Ser	gtg Val	aat Asn	gga Gly	ctc Leu 460	tgt Cys	gtc Val	cct Pro	gcc Ala	tgt Cys 465	gat Asp	ggg Gly	gtc Val	aag Lys	gac Asp 470	tgc Cys	1445
ccc Pro	aac Asn	ggc Gly	ctg Leu	gat Asp	gag Glu	aga Arg	aac Asn	tgc Cys 480	gtt Val	tgc Cys	aga Arg	gcc Ala	aca Thr 485	ttc Phe	cag Gln	1493
tgc Cys	aaa Lys	gag Glu	gac Asp	agc Ser	aca Thr	tgc Cys 495	atc Ile	tca Ser	ctg Leu	ccc Pro	aag Lys	gtc Val	tgt Cys	gat Asp	ggg Gly	1541
cag Gln 505	cct Pro	gat Asp	tgt Cys	ctc Leu	aac Asn	ggc Gly 510	agc Ser	gac Asp	gaa Glu	gag Glu	cag Gln 515	tgc Cys	cag Gln	gaa Glu	ggg Gly	1589
gtg Val 520	cca Pro	tgt Cys	ggg Gly	aca Thr	ttc Phe 525	acc Thr	ttc Phe	cag Gln	tgt Cys	gag Glu	gac Asp	cgg Arg	agc Ser	tgc Cys	gtg Val 535	1637
aag Lys	aag Lys	ccc Pro	aac Asn	ccg Pro 540	cag Gln	tgt Cys	gat Asp	ggg Gly	cgg Arg 545	ccc Pro	gac Asp	tgc Cys	agg Arg	gac Asp 550	ggc Gly	1685
tcg Ser	gat Asp	gag Glu	gag Glu	cac His 555	tgt Cys	gaa Glu	tgt Cys	ggc Gly 560	ctc Leu	cag Gln	ggc Gly	ccc Pro	tcc Ser 565	agc Ser	cgc Arg	1733
att Ile	gtt Val	ggt Gly 570	gga Gly	gct Ala	gtg Val	tcc Ser 575	tcc Ser	gag Glu	ggt Gly	gag Glu	tgg Trp 580	cca Pro	tgg Trp	cag Gln	gcc Ala	1781
agc Ser 585	ctc Leu	cag Gln	gtt Val	cgg Arg	ggt Gly	cga Arg 590	cac His	atc Ile	tgt Cys	ggg Gly	ggg Gly 595	gcc Ala	ctc Leu	atc Ile	gct Ala	1829
gac Gln	cgc Trp	tgg Glu	gtg Ala	ata Gln	aca Glu	gct Glu	gcc Gln	cac Glu	tgc Cys	ttc Gln	cag Glu	gag Glu	gac Glu	agc Glu	atg Glu	1877

[illegible]

-16-

tgccctttgg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa

3104

<210> 8

<211> 802

<212> PRT

<213> Homo Sapien

<400> 8

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	Gly
1				5					10					15	
Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	Cys	Glu
			20					25					30		
Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	Pro	Leu	Phe
		35					40					45			
Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	Val	Leu	Leu	Trp
	50					55					60				
Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	Ser	Gln	Val	Tyr	Ser
65					70					75				80	
Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	Ser	Gln	Asp	Leu	Thr	Arg
				85					90					95	
Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	Thr	Ala	Lys	Ala	Gln	Lys	Met
			100					105					110		
Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser
		115					120					125			
Ser	Ser	Val	Tyr	Ser	Phe	Gly	Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp
	130					135					140				
Phe	Ile	Leu	Gln	Ile	Pro	Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu
145					150					155					160
Val	Val	Gln	Ala	Leu	Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser
				165					170					175	
Ser	Ala	Ala	Val	Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly
			180					185					190		
Leu	Val	Ile	Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser
	195						200					205			
Thr	Leu	Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu
	210					215					220				
Arg	Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu
225					230					235					240
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	Leu
				245					250					255	
Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	Pro	Leu
			260					265					270		
Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	Gln	Glu	Pro
		275					280					285			
Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala	Val	Val	Trp	Lys
	290					295					300				
Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val	Leu	Ser	Val	Gln	Pro
305					310					315					320
Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu	Thr	Leu	Asp	Asn	Arg	Leu
				325					330					335	
Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro	Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser
			340					345					350		
Pro	Gln	Thr	His	Cys	Ser	Trp	His	Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr
		355					360					365			
Gly	Leu	Ala	Leu	Trp	Phe	Asp	Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr
	370					375					380				
Asp	Leu	Pro	Cys	Thr	Gln	Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu
385					390					395					400
Cys	Gly	Leu	Arg	Ile	Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val
				405					410					415	
Ala	Thr	Ala	Gly	Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr

-17-

			420					425					430				
Gly	Pro	Gly	Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro		
		435					440					445					
Cys	Pro	Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala		
	450					455					460						
Cys	Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys		
465					470					475					480		
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser		
			485						490					495			
Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp		
			500					505					510				
Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln		
		515					520					525					
Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly		
	530					535				540							
Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly		
545					550				555						560		
Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu		
			565						570						575		
Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile		
			580					585					590				
Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His		
	595					600					605						
Cys	Phe	Gln	Glu	Asp	Ser	Met	Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe		
	610					615				620							
Leu	Gly	Lys	Val	Trp	Gln	Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe		
625					630				635						640		
Lys	Val	Ser	Arg	Leu	Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His		
			645					650						655			
Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser		
			660					665					670				
Ala	Ala	Val	Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu		
		675					680					685					
Pro	Gly	Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly		
	690					695					700						
Gly	Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro		
705					710					715					720		
Gln	Asp	Leu	Cys	Ser	Glu	Val	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg	Met		
			725						730					735			
Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln	Gly	Asp		
			740					745					750				
Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg	Trp	Phe	Leu		
	755						760					765					
Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg	Pro	Asn	Tyr	Phe		
	770					775					780						
Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser	Trp	Ile	Gln	Gln	Val		
785					790					795					800		
Val	Thr																

<210> 9

<211> 2672

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (33)...(2009)

<223> cDNA encoding: MTSP4-S (short form) splice variant

<400> 9

-18-

tcacgcggcca gaggggtgac agtgagcaga ag	atg ccc gtg gcc gag gcc ccc	53
	Met Pro Val Ala Glu Ala Pro	
	1 5	
cag gtg gct ggc ggg cag ggg gac gga ggt gat ggc gag gaa gcg gag	101	
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu		
	10 15 20	
ccg gag ggg atg ttc aag gcc tgt gag gac tcc aag aga aaa gcc cgg	149	
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg		
	25 30 35	
ggc tac ctc cgc ctg gtg ccc ctg ttt gtg ctg ctg gcc ctg ctc gtg	197	
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val		
	40 45 50 55	
ctg gct tcg gcg ggg gtg cta ctc tgg tat ttc cta ggg tac aag gcg	245	
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala		
	60 65 70	
gag gtg atg gtc agc cag gtg tac tca ggc agt ctg cgt gta ctc aat	293	
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn		
	75 80 85	
cgc cac ttc tcc cag gat ctt acc cgc cgg gaa tct agt gcc ttc cgc	341	
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg		
	90 95 100	
agt gaa acc gcc aaa gcc cag aag atg ctc aag gag ctc atc acc agc	389	
Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser		
	105 110 115	
acc cgc ctg gga act tac tac aac tcc agc tcc gtc tat tcc ttt ggg	437	
Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Val Tyr Ser Phe Gly		
	120 125 130 135	
gtg tac ggc tgc agc cgc cag gag ccc gtg gtg gag gtt ctg gcg tcg	485	
Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser		
	140 145 150	
ggg gcc atc atg gcg gtc gtc tgg aag aag ggc ctg cac agc tac tac	533	
Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr		
	155 160 165	
gac ccc ttc gtg ctc tcc gtg cag ccg gtg gtc ttc cag gcc tgt gaa	581	
Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu		
	170 175 180	
gtg aac ctg acg ctg gac aac agg ctc gac tcc cag ggc gtc ctc agc	629	
Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser		
	185 190 195	
acc ccg tac ttc ccc agc tac tac tcg ccc caa acc cac tgc tcc tgg	677	
Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp		
	200 205 210 215	
cac ctc acg gtg ccc tct ctg gac tac ggc ttg gcc ctc tgg ttt gat	725	
His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp		
	220 225 230	
gcc tat gca ctg agg agg cag aag tat gat ttg ccg tgc acc cag gcc	773	

-19-

Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr	Asp	Leu	Pro	Cys	Thr	Gln	Gly		
			235					240					245				
cag	tgg	acg	atc	cag	aac	agg	agg	ctg	tgt	ggc	ttg	cgc	atc	ctg	cag	821	
Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile	Leu	Gln		
		250				255				260							
ccc	tac	gcc	gag	agg	atc	ccc	gtg	gtg	gcc	acg	gcc	ggg	atc	acc	atc	869	
Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly	Ile	Thr	Ile		
	265					270				275							
aac	ttc	acc	tcc	cag	atc	tcc	ctc	acc	ggg	ccc	ggt	gtg	cgg	gtg	cac	917	
Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly	Val	Arg	Val	His		
280					285				290						295		
tat	ggc	ttg	tac	aac	cag	tcg	gac	ccc	tgc	cct	gga	gag	ttc	ctc	tgt	965	
Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro	Gly	Glu	Phe	Leu	Cys		
				300				305						310			
tct	gtg	aat	gga	ctc	tgt	gtc	cct	gcc	tgt	gat	ggg	gtc	aag	gac	tgc	1013	
Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys	Asp	Gly	Val	Lys	Asp	Cys		
		315					320						325				
ccc	aac	ggc	ctg	gat	gag	aga	aac	tgc	gtt	tgc	aga	gcc	aca	ttc	cag	1061	
Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys	Val	Cys	Arg	Ala	Thr	Phe	Gln		
		330					335					340					
tgc	aaa	gag	gac	agc	aca	tgc	atc	tca	ctg	ccc	aag	gtc	tgt	gat	ggg	1109	
Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly		
	345					350				355							
cag	cct	gat	tgt	ctc	aac	ggc	agc	gac	gaa	gag	cag	tgc	cag	gaa	ggg	1157	
Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly		
360					365				370					375			
gtg	cca	tgt	ggg	aca	ttc	acc	ttc	cag	tgt	gag	gac	cgg	agc	tgc	gtg	1205	
Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val		
				380				385						390			
aag	aag	ccc	aac	ccg	cag	tgt	gat	ggg	cgg	ccc	gac	tgc	agg	gac	ggc	1253	
Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly		
			395				400					405					
tcg	gat	gag	gag	cac	tgt	gaa	tgt	ggc	ctc	cag	ggc	ccc	tcc	agc	cgc	1301	
Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg		
		410				415						420					
att	gtt	ggt	gga	gct	gtg	tcc	tcc	gag	ggt	gag	tgg	cca	tgg	cag	gcc	1349	
Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala		
	425					430				435							
agc	ctc	cag	gtt	cgg	ggt	cga	cac	atc	tgt	ggg	ggg	gcc	ctc	atc	gct	1397	
Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala		
440					445				450					455			
gac	cgc	tgg	gtg	ata	aca	gct	gcc	cac	tgc	ttc	cag	gag	gac	agc	atg	1445	
Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met		
				460					465					470			
gcc	tcc	acg	gtg	ctg	tgg	acc	gtg	ttc	ctg	ggc	aag	gtg	tgg	cag	aac	1493	
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln	Asn		

-20-

475	480	485	
tcg cgc tgg cct gga gag gtg tcc ttc aag gtg agc cgc ctg ctc ctg			1541
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu			
490	495	500	
cac ccg tac cac gaa gag gac agc cat gac tac gac gtg gcg ctg ctg			1589
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu			
505	510	515	
cag ctc gac cac ccg gtg gtg cgc tgc gcc gcc gtg cgc ccc gtc tgc			1637
Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys			
520	525	530	535
ctg ccc gcg cgc tcc cac ttc ttc gag ccc gcc ctg cac tgc tgg att			1685
Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile			
	540	545	550
acg gcc tgg gcc gcc ttg cgc gag gcc gcc ccc atc agc aac gct ctg			1733
Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu			
	555	560	565
cag aaa gtg gat gtg cag ttg atc cca cag gac ctg tgc agc gag gtc			1781
Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val			
	570	575	580
tat cgc tac cag gtg acg cca cgc atg ctg tgt gcc gcc tac cgc aag			1829
Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys			
	585	590	595
ggc aag aag gat gcc tgt cag ggt gac tca ggt ggt ccg ctg gtg tgc			1877
Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys			
600	605	610	615
aag gca ctc agt gcc cgc tgg ttc ctg gcg ggg ctg gtc agc tgg gcc			1925
Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly			
	620	625	630
ctg gcc tgt gcc cgg cct aac tac ttc gcc gtc tac acc cgc atc aca			1973
Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr			
	635	640	645
ggt gtg atc agc tgg atc cag caa gtg gtg acc tga ggaactgccc			2019
Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr *			
650	655		
ccctgcaaag cagggcccac ctccctggact cagagagccc agggcaactg ccaagcaggg			2079
ggacaagtat tctggcgggg ggtgggggag agagcaggcc ctgtggtggc aggaggggca			2139
tcttggttgc tccctgatgt ctgtccagta tggcaggagg atgagaagtg ccagcagttg			2199
gggggtcaaga cgtcccttga ggacccaggc ccacacccag cccttttgcc tcccaattct			2259
ctctcctccg tccccttcct ccactgctgc ctaatgcaag gcagtggctc agcagcaaga			2319
atgctgggtc tacatcccga ggagtgtctg aggtgcgccc cactctgtac agaggctgtt			2379
tgggcagcct tgcctccaga gagcagattc cagcttgcga agcccctggg ctaacttggg			2439
atctgggaat ggaaggtgct cccatcggag gggaccctca gagccctgga gactgccagg			2499
tgggcctgct gccactgtaa gccaaaaggt ggggaagtcc tgactccagg gtccttgccc			2559
cacccctgcc tgccacctgg gccctcacag cccagaccct cactgggagg tgagctcagc			2619
tgcccttttg aataaagctg cctgatgcaa aaaaaaaaaa aaaaaaaaaa aaa			2672
<210> 10			
<211> 658			
<212> PRT			

-21-

<213> Homo Sapien

<400> 10

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	Gly
1				5					10					15	
Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	Cys	Glu
			20					25					30		
Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	Pro	Leu	Phe
		35					40					45			
Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	Val	Leu	Leu	Trp
	50					55					60				
Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	Ser	Gln	Val	Tyr	Ser
65				70						75				80	
Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	Ser	Gln	Asp	Leu	Thr	Arg
				85					90					95	
Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	Thr	Ala	Lys	Ala	Gln	Lys	Met
			100					105					110		
Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser
		115					120					125			
Ser	Ser	Val	Tyr	Ser	Phe	Gly	Val	Tyr	Gly	Cys	Ser	Arg	Gln	Glu	Pro
	130					135					140				
Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala	Val	Val	Trp	Lys
145					150					155					160
Lys	Gly	Leu	His	Ser	Tyr	Tyr	Asp	Pro	Phe	Val	Leu	Ser	Val	Gln	Pro
				165					170					175	
Val	Val	Phe	Gln	Ala	Cys	Glu	Val	Asn	Leu	Thr	Leu	Asp	Asn	Arg	Leu
			180					185					190		
Asp	Ser	Gln	Gly	Val	Leu	Ser	Thr	Pro	Tyr	Phe	Pro	Ser	Tyr	Tyr	Ser
		195					200					205			
Pro	Gln	Thr	His	Cys	Ser	Trp	His	Leu	Thr	Val	Pro	Ser	Leu	Asp	Tyr
	210					215					220				
Gly	Leu	Ala	Leu	Trp	Phe	Asp	Ala	Tyr	Ala	Leu	Arg	Arg	Gln	Lys	Tyr
225					230					235					240
Asp	Leu	Pro	Cys	Thr	Gln	Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu
				245					250					255	
Cys	Gly	Leu	Arg	Ile	Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val
			260					265					270		
Ala	Thr	Ala	Gly	Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr
		275					280					285			
Gly	Pro	Gly	Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro
	290					295					300				
Cys	Pro	Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala
305					310					315					320
Cys	Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys
				325					330					335	
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile	Ser
			340					345					350		
Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly	Ser	Asp
		355					360					365			
Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe	Thr	Phe	Gln
	370					375					380				
Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro	Gln	Cys	Asp	Gly
385					390					395					400
Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu	His	Cys	Glu	Cys	Gly
				405					410					415	
Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly	Gly	Ala	Val	Ser	Ser	Glu
			420					425					430		
Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Val	Arg	Gly	Arg	His	Ile
		435					440					445			
Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp	Arg	Trp	Val	Ile	Thr	Ala	Ala	His
	450					455					460				

-22-

Cys Phe Gln Glu Asp Ser Met Ala Ser Thr Val Leu Trp Thr Val Phe
 465 470 475 480
 Leu Gly Lys Val Trp Gln Asn Ser Arg Trp Pro Gly Glu Val Ser Phe
 485 490 495
 Lys Val Ser Arg Leu Leu Leu His Pro Tyr His Glu Glu Asp Ser His
 500 505 510
 Asp Tyr Asp Val Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser
 515 520 525
 Ala Ala Val Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu
 530 535 540
 Pro Gly Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly
 545 550 555 560
 Gly Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro
 565 570 575
 Gln Asp Leu Cys Ser Glu Val Tyr Arg Tyr Gln Val Thr Pro Arg Met
 580 585 590
 Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln Gly Asp
 595 600 605
 Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg Trp Phe Leu
 610 615 620
 Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg Pro Asn Tyr Phe
 625 630 635 640
 Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser Trp Ile Gln Gln Val
 645 650 655
 Val Thr

<210> 11

<211> 1656

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (268)...(1629)

 <223> Nucleic acid encoding a transmembrane serine
 protease (MTSP-6) protein

<400> 11

cgcccgggca ggtagtaac actgtggcct actatctctt cagtgggtgcc atctacattt 60
 ttgggactcg ggaattatga ctgtttttgg ttaatcgata ctgaatgcgc tttgtgtgga 120
 ctgtcgaatt tcaaagattt accgtatgac caagatgcac ctgatgctac aagtataaat 180
 aggggaacaa atgctttctg ttcttcctcg gctaaggagg tagaggtgga ggaggagccg 240
 gatgtcagag gtcctgaaat agtcacc atg ggg gaa aat gat ccg cct gct gtt 294
 Met Gly Glu Asn Asp Pro Pro Ala Val
 1 5

 gaa gcc ccc ttc tca ttc cga tcg ctt ttt ggc ctt gat gat ttg aaa 342
 Glu Ala Pro Phe Ser Phe Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys 25
 10 15 20

 ata agt cct gtt gca cca gat gca gat gct gtt gct gca cag atc ctg 390
 Ile Ser Pro Val Ala Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu 40
 30 35 40

 tca ctg ctg cca ttg aag ttt ttt cca atc atc gtc att ggg atc att 438
 Ser Leu Leu Pro Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile 55
 45 50 55

 gca ttg ata tta gca ctg gcc att ggt ctg ggc atc cac ttc gac tgc 486
 Ala Leu Ile Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys

-23-

60					65					70						
tca	ggg	aag	tac	aga	tgt	cgc	tca	tcc	ttt	aag	tgt	atc	gag	ctg	ata	534
Ser	Gly	Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	
	75					80					85					
gct	cga	tgt	gac	gga	gtc	tcg	gat	tgc	aaa	gac	ggg	gag	gac	gag	tac	582
Ala	Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr	
90					95				100						105	
cgc	tgt	gtc	cgg	gtg	ggg	ggg	cag	aat	gcc	gtg	ctc	cag	gtg	ttc	aca	630
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe	Thr	
				110					115					120		
gct	gct	tcg	tgg	aag	acc	atg	tgc	tcc	gat	gac	tgg	aag	ggg	cac	tac	678
Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly	His	Tyr	
			125					130					135			
gca	aat	gtt	gcc	tgt	gcc	caa	ctg	ggg	ttc	cca	agc	tat	gta	agt	tca	726
Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr	Val	Ser	Ser	
		140					145					150				
gat	aac	ctc	aga	gtg	agc	tcg	cta	gag	ggg	cag	ttc	cgg	gag	gag	ttt	774
Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe	Arg	Glu	Glu	Phe	
	155					160					165					
gtg	tcc	atc	gat	cac	ctc	ttg	cca	gat	gac	aag	gtg	act	gca	tta	cac	822
Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys	Val	Thr	Ala	Leu	His	
170					175					180					185	
cac	tca	gta	tat	gtg	agg	gag	gga	tgt	gcc	tct	ggc	cac	gtg	gtt	acc	870
His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala	Ser	Gly	His	Val	Val	Thr	
				190					195					200		
ttg	cag	tgc	aca	gcc	tgt	ggg	cat	aga	agg	ggc	tac	agc	tca	cgc	atc	918
Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg	Arg	Gly	Tyr	Ser	Ser	Arg	Ile	
			205					210					215			
gtg	ggg	gga	aac	atg	tcc	ttg	ctc	tcg	cag	tgg	ccc	tgg	cag	gcc	agc	966
Val	Gly	Gly	Asn	Met	Ser	Leu	Leu	Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	
		220					225					230				
ctt	cag	ttc	cag	ggc	tac	cac	ctg	tgc	ggg	ggc	tct	gtc	atc	acg	ccc	1014
Leu	Gln	Phe	Gln	Gly	Tyr	His	Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	
	235					240					245					
ctg	tgg	atc	atc	act	gct	gca	cac	tgt	gtt	tat	gac	ttg	tac	ctc	ccc	1062
Leu	Trp	Ile	Ile	Thr	Ala	Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	
250					255					260					265	
aag	tca	tgg	acc	atc	cag	gtg	ggg	cta	gtt	tcc	ctg	ttg	gac	aat	cca	1110
Lys	Ser	Trp	Thr	Ile	Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	
				270				275						280		
gcc	cca	tcc	cac	ttg	gtg	gag	aag	att	gtc	tac	cac	agc	aag	tac	aag	1158
Ala	Pro	Ser	His	Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	
			285					290					295			
cca	aag	agg	ctg	ggc	aat	gac	atc	gcc	ctt	atg	aag	ctg	gcc	ggg	cca	1206
Pro	Lys	Arg	Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	
		300					305					310				

-24-

ctc acg ttc aat gaa atg atc cag cct gtg tgc ctg ccc aac tct gaa 1254
 Leu Thr Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu
 315 320 325

gag aac ttc ccc gat gga aaa gtg tgc tgg acg tca gga tgg ggg gcc 1302
 Glu Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala
 330 335 340 345

aca gag gat gga ggt gac gcc tcc cct gtc ctg aac cac gcg gcc gtc 1350
 Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val
 350 355 360

cct ttg att tcc aac aag atc tgc aac cac agg gac gtg tac ggt ggc 1398
 Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly
 365 370 375

atc atc tcc ccc tcc atg ctc tgc gcg ggc tac ctg acg ggt ggc gtg 1446
 Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val
 380 385 390

gac agc tgc cag ggg gac agc ggg ggg ccc ctg gtg tgt caa gag agg 1494
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg
 395 400 405

agg ctg tgg aag tta gtg gga gcg acc agc ttt ggc atc ggc tgc gca 1542
 Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala
 410 415 420 425

gag gtg aac aag cct ggg gtg tac acc cgt gtc acc tcc ttc ctg gac 1590
 Glu Val Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp
 430 435 440

tgg atc cac gag cag atg gag aga gac cta aaa acc tga agaggaaggg 1639
 Trp Ile His Glu Gln Met Glu Arg Asp Leu Lys Thr *
 445 450

gataagtagc cacctga 1656

<210> 12
 <211> 453
 <212> PRT
 <213> Homo Sapien

<400> 12
 Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
 1 5 10 15
 Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
 20 25 30
 Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
 35 40 45
 Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
 50 55 60
 Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
 65 70 75 80
 Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
 85 90 95
 Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
 100 105 110
 Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
 115 120 125

-25-

Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
 130 135 140
 Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
 145 150 155 160
 Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
 165 170 175
 Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
 180 185 190
 Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
 195 200 205
 His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
 210 215 220
 Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
 225 230 235 240
 Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
 245 250 255
 His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
 260 265 270
 Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
 275 280 285
 Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
 290 295 300
 Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
 305 310 315 320
 Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
 325 330 335
 Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Gly Asp Ala
 340 345 350
 Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys Ile
 355 360 365
 Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met Leu
 370 375 380
 Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp Ser
 385 390 395 400
 Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly
 405 410 415
 Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val
 420 425 430
 Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu
 435 440 445
 Arg Asp Leu Lys Thr
 450

<210> 13
 <211> 2100
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (45)...(1361)
 <223> Nucleic acid encoding MTSP7

<400> 13
 agatcagatg gcgactgaat agaagctgcc ccagtcctgg gttc atg atg tac aca
 Met Met Tyr Thr
 1

56

cct gtt gaa ttt tca gaa gct gaa ttc tca cga got gaa tat caa aga
 Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5 10 15 20

104

-26-

aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca	152
Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala	
25 30 35	
att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt	200
Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val	
40 45 50	
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca	248
Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr	
55 60 65	
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt	296
Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe	
70 75 80	
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga	344
Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg	
85 90 95 100	
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta	392
His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu	
105 110 115	
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga	440
Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg	
120 125 130	
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag	488
Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys	
135 140 145	
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac	536
Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn	
150 155 160	
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat	584
Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn	
165 170 175 180	
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca	632
Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro	
185 190 195	
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca	680
Leu Pro Ala Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr	
200 205 210	
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg	728
Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly	
215 220 225	
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc	776
Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu	
230 235 240	
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att	824
Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile	
245 250 255 260	

-27-

gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val	872
265 270 275	
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu Thr Asn Glu Asn	920
280 285 290	
gac att gct ttg gtt cag ctc tct act gga gtt gag ttt tca aat ata Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu Phe Ser Asn Ile	968
295 300 305	
gtc cag aga gtt tgc ctc cca gac tca tct ata aag ttg cca cct aaa Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys Leu Pro Pro Lys	1016
310 315 320	
aca agt gtg ttc gtc aca gga ttt gga tcc att gta gat gat gga cct Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val Asp Asp Gly Pro	1064
325 330 335 340	
ata caa aat aca ctt cgg caa gcc aga gtg gaa acc ata agc act gat Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr Ile Ser Thr Asp	1112
345 350 355	
gtg tgt aac aga aag gat gtg tat gat ggc ctg ata act cca gga atg Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile Thr Pro Gly Met	1160
360 365 370	
tta tgt gct gga ttc atg gaa gga aaa ata gat gca tgt aag gga gat Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala Cys Lys Gly Asp	1208
375 380 385	
tct ggt gga cct ctg gtt tat gat aat cat gac atc tgg tac att gta Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile Trp Tyr Ile Val	1256
390 395 400	
ggt ata gta agt tgg gga caa tca tgt gca ctt ccc aaa aaa cct gga Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro Lys Lys Pro Gly	1304
405 410 415 420	
gtc tac acc aga gta act aag tat cga gat tgg att gcc tca aag act Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile Ala Ser Lys Thr	1352
425 430 435	
ggt atg tag tgtggattgt ccatgagtta tacacatggc acacagagct Gly Met *	1401
gatactcctg cgtatTTTTgt attgttttaaa ttcattttact ttggatttagt gctttttgcta	1461
gatgtcaaga agcccttcag acccagacaa atctaataatc ctgaggtggc cttttacatac	1521
gtaggaccaa accctctcta ccatgagggga agaagacaca gcaaatgaca gacagcacct	1581
attccttact cacaagggaa actgcttgtg atactttccta ataagataaa taagtggttt	1641
ccctcaattg aagacaggaa catcattttc cacaggatat gaagagctgc cagtaatgcc	1701
aaaatcttac ctcatataat acctggagca tgtgagattc ttctagttaa aaagaacagt	1761
cttccctgaa gactcagggc ttcaacattc tagaactgat aagtggacct tcagtgtgca	1821
agaatggaga agcatgggat ttgcattatg acttgaactg ggcttatatc taataatata	1881
gagcactatc actaacctca acagttgaca ttttaaaagt ttttaaagt atctgaactt	1941
gctgttaaca cagtgttata actcaagcac tagcttcagg aagcatgttg tgttgtaag	2001
aagcttttct gatttattct ttaacagcat cttgccatct atatgttagt agcagttggc	2061
ccagaaagga caaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2100

-28-

<210> 14
 <211> 438
 <212> PRT
 <213> Homo sapien

<400> 14
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
 1 5 10 15
 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met

-29-

435

<210> 15
 <211> 702
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (1)...(702)
 <223> Nucleotide sequence encoding MTSP-7 Protease Domain

<400> 15
 att gtc caa gga agg gaa aca gct atg gaa ggg gaa tgg cca tgg cag 48
 Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15

gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc 96
 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30

atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat 144
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45

aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca 192
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60

ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac 240
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80

cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act 288
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95

gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca 336
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110

tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga 384
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125

tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga 432
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140

gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat 480
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160

ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa 528
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175

ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat 576
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190

-30-

```

cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt      624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
      195                      200                      205

```

```

gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga      672
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
      210                      215                      220

```

```

gat tgg att gcc tca aag act ggt atg tag      702
Asp Trp Ile Ala Ser Lys Thr Gly Met *
      225                      230

```

```

<210> 16
<211> 233
<212> PRT
<213> Homo sapien

```

```

<400> 16
Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1      5      10      15
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
      20      25      30
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
      35      40      45
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
      50      55      60
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
      65      70      75      80
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
      85      90      95
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
      100      105      110
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
      115      120      125
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
      130      135      140
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
      145      150      155      160
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
      165      170      175
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
      180      185      190
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
      195      200      205
Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
      210      215      220
Asp Trp Ile Ala Ser Lys Thr Gly Met
      225      230

```

```

<210> 17
<211> 777
<212> DNA
<213> Homo Sapien

```

```

<220>
<221> CDS
<222> (1)...(729)
<223> Nucleotide sequence encoding MTSP9, including
      protease domain (31-729)

```


-31-

<400> 17
 aaa cga gtt gtt cca tta aac gtc aac aga ata gca tct gga gtc att 48
 Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
 1 5 10 15

gca ccc aag gcg gcc tgg cct tgg caa gct tcc ctt cag tat gat aac 96
 Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
 20 25 30

atc cat cag tgt ggg gcc acc ttg att agt aac aca tgg ctt gtc act 144
 Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
 35 40 45

gca gca cac tgc ttc cag aag tat aaa aat cca cat caa tgg act gtt 192
 Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
 50 55 60

agt ttt gga aca aaa atc aac cct ccc tta atg aaa aga aat gtc aga 240
 Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
 65 70 75 80

aga ttt att atc cat gag aag tac cgc tct gca gca aga gag tac gac 288
 Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
 85 90 95

att gct gtt gtg cag gtc tct tcc aga gtc acc ttt tcg gat gac ata 336
 Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
 100 105 110

cgc cgg att tgt ttg cca gaa gcc tct gca tcc ttc caa cca aat ttg 384
 Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
 115 120 125

act gtc cac atc aca gga ttt gga gca ctt tac tat ggt ggg gaa tcc 432
 Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
 130 135 140

caa aat gat ctc cga gaa gcc aga gtg aaa atc ata agt gac gat gtc 480
 Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
 145 150 155 160

tgc aag caa cca cag gtg tat ggc aat gat ata aaa cct gga atg ttc 528
 Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
 165 170 175

tgt gcc gga tat atg gaa gga att tat gat gcc tgc agg ggt gat tct 576
 Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
 180 185 190

ggg gga cct tta gtc aca agg gat ctg aaa gat acg tgg tat ctc att 624
 Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
 195 200 205

gga att gta agc tgg gga gat aac tgt ggt caa aag gac aag cct gga 672
 Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
 210 215 220

gtc tac aca caa gtg act tat tac cga aac tgg att gct tca aaa aca 720
 Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
 225 230 235 240

-32-

ggc atc taa ttcacgataa aagttaaaca aagaaagctg tatgcaggtc atatatgc 777
Gly Ile

<210> 18

<211> 242

<212> PRT

<213> Homo Sapien

<220>

<221> SITE

<222> (11)...(242)

<223> MTSP9 protease domain

<400> 18

Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
1 5 10 15

Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
20 25 30

Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
35 40 45

Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
50 55 60

Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
65 70 75 80

Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
85 90 95

Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
100 105 110

Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
115 120 125

Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
130 135 140

Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
145 150 155 160

Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
165 170 175

Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
180 185 190

Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
195 200 205

Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
210 215 220

Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
225 230 235 240

Gly Ile

-33-

<210> 19 MTSP12
 <211> 3316
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1)...(3282)
 <223> Nucleotide sequence encoding MTSP12, including
 MTSP12-PD1, MTSP12-PD2, and MTSP12-PD3 protease
 domains

<400> 19
 atg gag ccc act gtg gct aac gta cac ctc gtg ccc agg aca acc aag 48
 Met Glu Pro Thr Val Ala Asn Val His Leu Val Pro Arg Thr Thr Lys
 1 5 10 15
 gaa gtc ccc gct ctg gat gcc gcg tgc tgt cga gcg gcc acc att ggc 96
 Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Thr Ile Gly
 20 25 30
 gtg gtg gcc acc agc ctt gtc gtc ctc acc ctg gga gtc ctt ttg gcc 144
 Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala
 35 40 45
 ttc ctc tct aca cag ggc ttc cac gtg gac cac acg gcc gag ctg cgg 192
 Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg
 50 55 60
 gga atc cgg tgg acc agc agt ttg cgg cgg gag acc tcg gac tat cac 240
 Gly Ile Arg Trp Thr Ser Ser Leu Arg Arg Glu Thr Ser Asp Tyr His
 65 70 75 80
 cgc acg ctg acg ccc acc ctg gag gca ctg ttt gta agt agt ttt cag 288
 Arg Thr Leu Thr Pro Thr Leu Glu Ala Leu Phe Val Ser Ser Phe Gln
 85 90 95
 aag aca gag tta gag gca agc tgc gtg ggt tgc tcg gta ctg aat tat 336
 Lys Thr Glu Leu Glu Ala Ser Cys Val Gly Cys Ser Val Leu Asn Tyr
 100 105 110
 agg gat ggg aac tcc agt gtc ctc gta cat ttc cag ctg cac ttt ctg 384
 Arg Asp Gly Asn Ser Ser Val Leu Val His Phe Gln Leu His Phe Leu
 115 120 125
 ctg cga ccc ctc cag acg ctg agc ctg ggc ctg gag gag gag cta ttg 432
 Leu Arg Pro Leu Gln Thr Leu Ser Leu Gly Leu Glu Glu Glu Leu Leu
 130 135 140
 cag cga ggg atc cgg gca agg ctg cgg gag cac ggc atc tcc ctg gct 480
 Gln Arg Gly Ile Arg Ala Arg Leu Arg Glu His Gly Ile Ser Leu Ala
 145 150 155 160
 gcc tat ggc aca att gtg tcg gct gag ctc aca ggg aga cat aag ggg 528
 Ala Tyr Gly Thr Ile Val Ser Ala Glu Leu Thr Gly Arg His Lys Gly
 165 170 175
 ccc ttg gca gaa aga gac ttc aaa tca ggc cgc tgt cca ggg aac tcc 576
 Pro Leu Ala Glu Arg Asp Phe Lys Ser Gly Arg Cys Pro Gly Asn Ser
 180 185 190

-34-

ttt tcc tgc ggg aac agc cag tgt gtg acc aag gtg aac ccg gag tgt	624
Phe Ser Cys Gly Asn Ser Gln Cys Val Thr Lys Val Asn Pro Glu Cys	
195 200 205	
gac gac cag gag gac tgc tcc gat ggg tcc gac gag gcg cac tgc gag	672
Asp Asp Gln Glu Asp Cys Ser Asp Gly Ser Asp Glu Ala His Cys Glu	
210 215 220	
tgt ggc ttg cag cct gcc tgg agg atg gcc ggc agg atc gtg ggc ggc	720
Cys Gly Leu Gln Pro Ala Trp Arg Met Ala Gly Arg Ile Val Gly Gly	
225 230 235 240	
atg gaa gca tcc ccg ggg gag ttt ccg tgg caa gcc agc ctt cga gag	768
Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala Ser Leu Arg Glu	
245 250 255	
aac aag gag cac ttc tgt ggg gcc gcc atc atc aac gcc agg tgg ctg	816
Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn Ala Arg Trp Leu	
260 265 270	
gtg tct gct gct cac tgc ttc aat gag ttc caa gac ccg acg aag tgg	864
Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp Pro Thr Lys Trp	
275 280 285	
gtg gcc tac gtg ggt gcg acc tac ctc agc ggc tgc gag gcc agc acc	912
Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser Glu Ala Ser Thr	
290 295 300	
gtg cgg gcc cag gtg gtc cag atc gtc aag cac ccc ctg tac aac gcg	960
Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro Leu Tyr Asn Ala	
305 310 315 320	
gac acg gcc gac ttt gac gtg gct gtg ctg gag ctg acc agc cct ctg	1008
Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu Thr Ser Pro Leu	
325 330 335	
cct ttc ggc cgg cac atc cag ccc gtg tgc ctc ccg gct gcc aca cac	1056
Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro Ala Ala Thr His	
340 345 350	
atc ttc cca ccc agc aag aag tgc ctg atc tca ggc tgg ggc tac ctc	1104
Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly Trp Gly Tyr Leu	
355 360 365	
aag gag gac ttc ctg gtc aag cca ggg gtg ctg cag aaa gcc act gtg	1152
Lys Glu Asp Phe Leu Val Lys Pro Gly Val Leu Gln Lys Ala Thr Val	
370 375 380	
gag ctg ctg gac cag gca ctg tgt gcc agc ttg tac ggc cat tca ctc	1200
Glu Leu Leu Asp Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu	
385 390 395 400	
act gac agg atg gtg tgc gct ggc tac ctg gac ggg aag gtg gac tcc	1248
Thr Asp Arg Met Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser	
405 410 415	
tgc cag ggt gac tca gga gga ccc ctg gtc tgc gag gag ccc tct ggc	1296
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly	
420 425 430	
cgg ttc tct ctg gct ggc atc gtg agc tgg gga atc ggg tgt gcg gaa	1344

-35-

Arg	Phe	Ser	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Ile	Gly	Cys	Ala	Glu	
		435					440					445				
gcc	cgg	cgt	cca	ggg	gtc	tat	gcc	cga	gtc	acc	agg	cta	cgt	gac	tgg	1392
Ala	Arg	Arg	Pro	Gly	Val	Tyr	Ala	Arg	Val	Thr	Arg	Leu	Arg	Asp	Trp	
	450					455					460					
atc	ctg	gag	gcc	acc	acc	aaa	gcc	agc	atg	cct	ctg	gcc	ccc	acc	atg	1440
Ile	Leu	Glu	Ala	Thr	Thr	Lys	Ala	Ser	Met	Pro	Leu	Ala	Pro	Thr	Met	
465					470					475					480	
gct	cct	gcc	cct	gcc	gcc	ccc	agc	aca	gcc	tgg	ccc	acc	agt	cct	gag	1488
Ala	Pro	Ala	Pro	Ala	Ala	Pro	Ser	Thr	Ala	Trp	Pro	Thr	Ser	Pro	Glu	
				485					490					495		
u																
agc	cct	gtt	gtc	agc	acc	ccc	acc	aaa	tcg	atg	cag	gcc	ctc	agt	acc	1536
Ser	Pro	Val	Val	Ser	Thr	Pro	Thr	Lys	Ser	Met	Gln	Ala	Leu	Ser	Thr	
		500						505					510			
gtg	cct	ctt	gac	tgg	gtc	acc	gtt	cct	aag	cta	caa	gaa	tgt	ggg	gcc	1584
Val	Pro	Leu	Asp	Trp	Val	Thr	Val	Pro	Lys	Leu	Gln	Glu	Cys	Gly	Ala	
		515					520					525				
agg	cct	gca	atg	gag	aag	ccc	acc	cgg	gtc	gtg	ggc	ggg	ttc	gga	gct	1632
Arg	Pro	Ala	Met	Glu	Lys	Pro	Thr	Arg	Val	Val	Gly	Gly	Phe	Gly	Ala	
	530					535					540					
gcc	tcc	ggg	gag	gtg	ccc	tgg	cag	gtc	agc	ctg	aag	gaa	ggg	tcc	cgg	1680
Ala	Ser	Gly	Glu	Val	Pro	Trp	Gln	Val	Ser	Leu	Lys	Glu	Gly	Ser	Arg	
545					550					555					560	
cac	ttc	tgc	gga	gca	act	gtg	gtg	ggg	gac	cgc	tgg	ctg	ctg	tct	gcc	1728
His	Phe	Cys	Gly	Ala	Thr	Val	Val	Gly	Asp	Arg	Trp	Leu	Leu	Ser	Ala	
			565						570					575		
gcc	cac	tgc	ttc	aac	cac	acg	aag	gtg	gag	cag	gtt	cgg	gcc	cac	ctg	1776
Ala	His	Cys	Phe	Asn	His	Thr	Lys	Val	Glu	Gln	Val	Arg	Ala	His	Leu	
			580					585					590			
ggc	act	gcg	tcc	ctc	ctg	ggc	ctg	ggc	ggg	agc	ccg	gtg	aag	atc	ggg	1824
Gly	Thr	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Gly	Ser	Pro	Val	Lys	Ile	Gly	
		595					600					605				
ctg	cgg	cgg	gta	gtg	ctg	cac	ccc	ctc	tac	aac	cct	ggc	atc	ctg	gac	1872
Leu	Arg	Arg	Val	Val	Leu	His	Pro	Leu	Tyr	Asn	Pro	Gly	Ile	Leu	Asp	
	610					615					620					
ttc	gac	ctg	gct	gtc	ctg	gag	ctg	gcc	agc	ccc	ctg	gcc	ttc	aac	aaa	1920
Phe	Asp	Leu	Ala	Val	Leu	Glu	Leu	Ala	Ser	Pro	Leu	Ala	Phe	Asn	Lys	
625					630					635					640	
tac	atc	cag	cct	gtc	tgc	ctg	ccc	ctg	gcc	atc	cgg	aag	ttc	cct	gtg	1968
Tyr	Ile	Gln	Pro	Val	Cys	Leu	Pro	Leu	Ala	Ile	Arg	Lys	Phe	Pro	Val	
				645					650					655		
ggc	cgg	aag	tgc	atg	atc	tcc	gga	tgg	gga	aat	acg	cag	gaa	gga	aat	2016
Gly	Arg	Lys	Cys	Met	Ile	Ser	Gly	Trp	Gly	Asn	Thr	Gln	Glu	Gly	Asn	
			660					665					670			
gcc	acc	aag	ccc	gag	ctc	ctg	cag	aag	gcg	tcc	gtg	ggc	atc	ata	gac	2064
Ala	Thr	Lys	Pro	Glu	Leu	Leu	Gln	Lys	Ala	Ser	Val	Gly	Ile	Ile	Asp	

-36-

675	680	685	
cag aaa acc tgt agt gtg ctc tac aac ttc tcc ctc aca gac cgc atg Gln Lys Thr Cys Ser Val Leu Tyr Asn Phe Ser Leu Thr Asp Arg Met 690 695 700			2112
atc tgc gca ggc ttc ctg gaa ggc aaa gtc gac tcc tgc cag ggt gac Ile Cys Ala Gly Phe Leu Glu Gly Lys Val Asp Ser Cys Gln Gly Asp 705 710 715 720			2160
tct ggg ggc ccc ctg gcc tgc gag gag gcc cct ggc gtg ttt tat ctg Ser Gly Gly Pro Leu Ala Cys Glu Glu Ala Pro Gly Val Phe Tyr Leu 725 730 735			2208
gca ggg atc gtg agc tgg ggt att ggc tgc gct cag gtt aag aag ccg Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Gln Val Lys Lys Pro 740 745 750			2256
ggc gtg tac acg cgc atc acc agg cta aag ggc tgg atc ctg gag atc Gly Val Tyr Thr Arg Ile Thr Arg Leu Lys Gly Trp Ile Leu Glu Ile 755 760 765			2304
atg tcc tcc cag ccc ctt ccc atg tct ccc ccc tcc acc aca agg atg Met Ser Ser Gln Pro Leu Pro Met Ser Pro Pro Ser Thr Thr Arg Met 770 775 780			2352
ctg gcc acc acc agc ccc agg acg aca gct ggc ctc aca gtc ccg ggg Leu Ala Thr Thr Ser Pro Arg Thr Thr Ala Gly Leu Thr Val Pro Gly 785 790 795 800			2400
gcc aca ccc agc aga ccc acc cct ggg gct gcc agc agg gtg acg ggc Ala Thr Pro Ser Arg Pro Thr Pro Gly Ala Ala Ser Arg Val Thr Gly 805 810 815			2448
caa cct gcc aac tca acc tta tot gcc gtg agc acc act gct agg gga Gln Pro Ala Asn Ser Thr Leu Ser Ala Val Ser Thr Thr Ala Arg Gly 820 825 830			2496
cag acg cca ttt cca gac gcc ccg gag gcc acc aca cac acc cag cta Gln Thr Pro Phe Pro Asp Ala Pro Glu Ala Thr Thr His Thr Gln Leu 835 840 845			2544
cca gac tgt ggc ctg gcg ccg gcc gcg ctc acc agg att gtg ggc ggc Pro Asp Cys Gly Leu Ala Pro Ala Ala Leu Thr Arg Ile Val Gly Gly 850 855 860			2592
agc gca gcg ggc cgt ggg gag tgg ccg tgg cag gtg ggc ctg tgg ctg Ser Ala Ala Gly Arg Gly Glu Trp Pro Trp Gln Val Gly Leu Trp Leu 865 870 875 880			2640
cgg cgc cgg gaa cac cgt tgc ggg gcc gtg ctg gtg gca gag agg tgg Arg Arg Arg Glu His Arg Cys Gly Ala Val Leu Val Ala Glu Arg Trp 885 890 895			2688
ctg ctg tcc gcg gcg cac tgc ttc gac gtc tac ggg gac ccc aag cag Leu Leu Ser Ala Ala His Cys Phe Asp Val Tyr Gly Asp Pro Lys Gln 900 905 910			2736
tgg gcg gcc ttc cta ggc acg ccg ttc ctg agc ggc gcg gag ggg cag Trp Ala Ala Phe Leu Gly Thr Pro Phe Leu Ser Gly Ala Glu Gly Gln 915 920 925			2784

-37-

ctg gag cgc gtg gcg cgc atc tac aag cac ccg ttc tac aat ctc tac	2832
Leu Glu Arg Val Ala Arg Ile Tyr Lys His Pro Phe Tyr Asn Leu Tyr	
930 935 940	
acg ctc gac tac gac gtg gcg ctt ctg gag ctg gcg ggg ccg gtg cgt	2880
Thr Leu Asp Tyr Asp Val Ala Leu Leu Glu Leu Ala Gly Pro Val Arg	
945 950 955 960	
cgc agc cgc ctg gtg cgt ccc atc tgc ctg ccc gag ccc gcg ccg cga	2928
Arg Ser Arg Leu Val Arg Pro Ile Cys Leu Pro Glu Pro Ala Pro Arg	
965 970 975	
ccc ccg gac ggc acg cgc tgc gtc atc acc ggc tgg ggc tcg gtg cgc	2976
Pro Pro Asp Gly Thr Arg Cys Val Ile Thr Gly Trp Gly Ser Val Arg	
980 985 990	
gaa gga ggc tcc atg gcg cgg cag ctg cag aag gcg gcc gtg cgc ctc	3024
Glu Gly Gly Ser Met Ala Arg Gln Leu Gln Lys Ala Ala Val Arg Leu	
995 1000 1005	
ctc agc gag cag acc tgc cgc cgc ttc tac cca gtg cag atc agc agc	3072
Leu Ser Glu Gln Thr Cys Arg Arg Phe Tyr Pro Val Gln Ile Ser Ser	
1010 1015 1020	
cgc atg ctg tgt gcc ggc ttc ccg cag ggt ggc gtg gac agc tgc tcg	3120
Arg Met Leu Cys Ala Gly Phe Pro Gln Gly Gly Val Asp Ser Cys Ser	
1025 1030 1035 1040	
ggt gac gct ggg gga ccc ctg gcc tgc agg gag ccc tct gga cgg tgg	3168
Gly Asp Ala Gly Gly Pro Leu Ala Cys Arg Glu Pro Ser Gly Arg Trp	
1045 1050 1055	
gtg cta act ggg gtc act agc tgg ggc tat ggc tgt ggc cgg ccc cac	3216
Val Leu Thr Gly Val Thr Ser Trp Gly Tyr Gly Cys Gly Arg Pro His	
1060 1065 1070	
ttc cca ggt gtc tat acc cgg gtg gca gct gtg aga ggc tgg ata gga	3264
Phe Pro Gly Val Tyr Thr Arg Val Ala Ala Val Arg Gly Trp Ile Gly	
1075 1080 1085	
cag cac atc cag gag tga ccaccacgtg actgcccagg ccgagactct	3312
Gln His Ile Gln Glu *	
1090	
acgt	3316
<210> 20	
<211> 1093	
<212> PRT	
<213> Homo Sapien	
<400> 20	
Met Glu Pro Thr Val Ala Asn Val His Leu Val Pro Arg Thr Thr Lys	
1 5 10 15	
Glu Val Pro Ala Leu Asp Ala Ala Cys Cys Arg Ala Ala Thr Ile Gly	
20 25 30	
Val Val Ala Thr Ser Leu Val Val Leu Thr Leu Gly Val Leu Leu Ala	
35 40 45	
Phe Leu Ser Thr Gln Gly Phe His Val Asp His Thr Ala Glu Leu Arg	
50 55 60	

-38-

Gly	Ile	Arg	Trp	Thr	Ser	Ser	Leu	Arg	Arg	Glu	Thr	Ser	Asp	Tyr	His
65					70					75					80
Arg	Thr	Leu	Thr	Pro	Thr	Leu	Glu	Ala	Leu	Phe	Val	Ser	Ser	Phe	Gln
				85					90					95	
Lys	Thr	Glu	Leu	Glu	Ala	Ser	Cys	Val	Gly	Cys	Ser	Val	Leu	Asn	Tyr
			100					105					110		
Arg	Asp	Gly	Asn	Ser	Ser	Val	Leu	Val	His	Phe	Gln	Leu	His	Phe	Leu
		115					120					125			
Leu	Arg	Pro	Leu	Gln	Thr	Leu	Ser	Leu	Gly	Leu	Glu	Glu	Glu	Leu	Leu
		130				135					140				
Gln	Arg	Gly	Ile	Arg	Ala	Arg	Leu	Arg	Glu	His	Gly	Ile	Ser	Leu	Ala
145					150					155					160
Ala	Tyr	Gly	Thr	Ile	Val	Ser	Ala	Glu	Leu	Thr	Gly	Arg	His	Lys	Gly
				165					170					175	
Pro	Leu	Ala	Glu	Arg	Asp	Phe	Lys	Ser	Gly	Arg	Cys	Pro	Gly	Asn	Ser
			180					185					190		
Phe	Ser	Cys	Gly	Asn	Ser	Gln	Cys	Val	Thr	Lys	Val	Asn	Pro	Glu	Cys
		195					200					205			
Asp	Asp	Gln	Glu	Asp	Cys	Ser	Asp	Gly	Ser	Asp	Glu	Ala	His	Cys	Glu
		210				215					220				
Cys	Gly	Leu	Gln	Pro	Ala	Trp	Arg	Met	Ala	Gly	Arg	Ile	Val	Gly	Gly
225					230					235					240
Met	Glu	Ala	Ser	Pro	Gly	Glu	Phe	Pro	Trp	Gln	Ala	Ser	Leu	Arg	Glu
				245					250					255	
Asn	Lys	Glu	His	Phe	Cys	Gly	Ala	Ala	Ile	Ile	Asn	Ala	Arg	Trp	Leu
			260					265					270		
Val	Ser	Ala	Ala	His	Cys	Phe	Asn	Glu	Phe	Gln	Asp	Pro	Thr	Lys	Trp
		275					280					285			
Val	Ala	Tyr	Val	Gly	Ala	Thr	Tyr	Leu	Ser	Gly	Ser	Glu	Ala	Ser	Thr
		290				295					300				
Val	Arg	Ala	Gln	Val	Val	Gln	Ile	Val	Lys	His	Pro	Leu	Tyr	Asn	Ala
305					310					315					320
Asp	Thr	Ala	Asp	Phe	Asp	Val	Ala	Val	Leu	Glu	Leu	Thr	Ser	Pro	Leu
				325					330					335	
Pro	Phe	Gly	Arg	His	Ile	Gln	Pro	Val	Cys	Leu	Pro	Ala	Ala	Thr	His
			340					345					350		
Ile	Phe	Pro	Pro	Ser	Lys	Lys	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Tyr	Leu
		355					360					365			
Lys	Glu	Asp	Phe	Leu	Val	Lys	Pro	Gly	Val	Leu	Gln	Lys	Ala	Thr	Val
		370				375					380				
Glu	Leu	Leu	Asp	Gln	Ala	Leu	Cys	Ala	Ser	Leu	Tyr	Gly	His	Ser	Leu
385					390					395					400
Thr	Asp	Arg	Met	Val	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Lys	Val	Asp	Ser
				405					410					415	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Glu	Glu	Pro	Ser	Gly
			420					425					430		
Arg	Phe	Ser	Leu	Ala	Gly	Ile	Val	Ser	Trp	Gly	Ile	Gly	Cys	Ala	Glu
			435				440					445			
Ala	Arg	Arg	Pro	Gly	Val	Tyr	Ala	Arg	Val	Thr	Arg	Leu	Arg	Asp	Trp
			450			455					460				
Ile	Leu	Glu	Ala	Thr	Thr	Lys	Ala	Ser	Met	Pro	Leu	Ala	Pro	Thr	Met
465					470					475					480
Ala	Pro	Ala	Pro	Ala	Ala	Pro	Ser	Thr	Ala	Trp	Pro	Thr	Ser	Pro	Glu
				485					490					495	
Ser	Pro	Val	Val	Ser	Thr	Pro	Thr	Lys	Ser	Met	Gln	Ala	Leu	Ser	Thr
			500					505					510		
Val	Pro	Leu	Asp	Trp	Val	Thr	Val	Pro	Lys	Leu	Gln	Glu	Cys	Gly	Ala
		515					520					525			
Arg	Pro	Ala	Met	Glu	Lys	Pro	Thr	Arg	Val	Val	Gly	Gly	Phe	Gly	Ala
		530				535					540				
Ala	Ser	Gly	Glu	Val	Pro	Trp	Gln	Val	Ser	Leu	Lys	Glu	Gly	Ser	Arg

-39-

545					550					555					560
His	Phe	Cys	Gly	Ala	Thr	Val	Val	Gly	Asp	Arg	Trp	Leu	Leu	Ser	Ala
				565					570						575
Ala	His	Cys	Phe	Asn	His	Thr	Lys	Val	Glu	Gln	Val	Arg	Ala	His	Leu
			580						585						590
Gly	Thr	Ala	Ser	Leu	Leu	Gly	Leu	Gly	Gly	Ser	Pro	Val	Lys	Ile	Gly
		595					600					605			
Leu	Arg	Arg	Val	Val	Leu	His	Pro	Leu	Tyr	Asn	Pro	Gly	Ile	Leu	Asp
	610					615					620				
Phe	Asp	Leu	Ala	Val	Leu	Glu	Leu	Ala	Ser	Pro	Leu	Ala	Phe	Asn	Lys
625					630					635					640
Tyr	Ile	Gln	Pro	Val	Cys	Leu	Pro	Leu	Ala	Ile	Arg	Lys	Phe	Pro	Val
				645					650						655
Gly	Arg	Lys	Cys	Met	Ile	Ser	Gly	Trp	Gly	Asn	Thr	Gln	Glu	Gly	Asn
			660					665					670		
Ala	Thr	Lys	Pro	Glu	Leu	Leu	Gln	Lys	Ala	Ser	Val	Gly	Ile	Ile	Asp
		675					680					685			
Gln	Lys	Thr	Cys	Ser	Val	Leu	Tyr	Asn	Phe	Ser	Leu	Thr	Asp	Arg	Met
	690					695					700				
Ile	Cys	Ala	Gly	Phe	Leu	Glu	Gly	Lys	Val	Asp	Ser	Cys	Gln	Gly	Asp
705					710					715					720
Ser	Gly	Gly	Pro	Leu	Ala	Cys	Glu	Glu	Ala	Pro	Gly	Val	Phe	Tyr	Leu
				725					730						735
Ala	Gly	Ile	Val	Ser	Trp	Gly	Ile	Gly	Cys	Ala	Gln	Val	Lys	Lys	Pro
			740					745					750		
Gly	Val	Tyr	Thr	Arg	Ile	Thr	Arg	Leu	Lys	Gly	Trp	Ile	Leu	Glu	Ile
		755					760					765			
Met	Ser	Ser	Gln	Pro	Leu	Pro	Met	Ser	Pro	Pro	Ser	Thr	Thr	Arg	Met
	770					775					780				
Leu	Ala	Thr	Thr	Ser	Pro	Arg	Thr	Thr	Ala	Gly	Leu	Thr	Val	Pro	Gly
785					790					795					800
Ala	Thr	Pro	Ser	Arg	Pro	Thr	Pro	Gly	Ala	Ala	Ser	Arg	Val	Thr	Gly
				805					810						815
Gln	Pro	Ala	Asn	Ser	Thr	Leu	Ser	Ala	Val	Ser	Thr	Thr	Ala	Arg	Gly
			820					825					830		
Gln	Thr	Pro	Phe	Pro	Asp	Ala	Pro	Glu	Ala	Thr	Thr	His	Thr	Gln	Leu
	835						840					845			
Pro	Asp	Cys	Gly	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Arg	Ile	Val	Gly	Gly
	850					855					860				
Ser	Ala	Ala	Gly	Arg	Gly	Glu	Trp	Pro	Trp	Gln	Val	Gly	Leu	Trp	Leu
865					870					875					880
Arg	Arg	Arg	Glu	His	Arg	Cys	Gly	Ala	Val	Leu	Val	Ala	Glu	Arg	Trp
				885					890						895
Leu	Leu	Ser	Ala	Ala	His	Cys	Phe	Asp	Val	Tyr	Gly	Asp	Pro	Lys	Gln
			900					905					910		
Trp	Ala	Ala	Phe	Leu	Gly	Thr	Pro	Phe	Leu	Ser	Gly	Ala	Glu	Gly	Gln
	915						920					925			
Leu	Glu	Arg	Val	Ala	Arg	Ile	Tyr	Lys	His	Pro	Phe	Tyr	Asn	Leu	Tyr
	930					935					940				
Thr	Leu	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Glu	Leu	Ala	Gly	Pro	Val	Arg
945					950					955					960
Arg	Ser	Arg	Leu	Val	Arg	Pro	Ile	Cys	Leu	Pro	Glu	Pro	Ala	Pro	Arg
				965					970						975
Pro	Pro	Asp	Gly	Thr	Arg	Cys	Val	Ile	Thr	Gly	Trp	Gly	Ser	Val	Arg
			980					985					990		
Glu	Gly	Gly	Ser	Met	Ala	Arg	Gln	Leu	Gln	Lys	Ala	Ala	Val	Arg	Leu
	995						1000					1005			
Leu	Ser	Glu	Gln	Thr	Cys	Arg	Arg	Phe	Tyr	Pro	Val	Gln	Ile	Ser	Ser
	1010					1015					1020				
Arg	Met	Leu	Cys	Ala	Gly	Phe	Pro	Gln	Gly	Gly	Val	Asp	Ser	Cys	Ser
1025					1030					1035					1040

-40-

Gly Asp Ala Gly Gly Pro Leu Ala Cys Arg Glu Pro Ser Gly Arg Trp
 1045 1050 1055
 Val Leu Thr Gly Val Thr Ser Trp Gly Tyr Gly Cys Gly Arg Pro His
 1060 1065 1070
 Phe Pro Gly Val Tyr Thr Arg Val Ala Ala Val Arg Gly Trp Ile Gly
 1075 1080 1085
 Gln His Ile Gln Glu
 1090

<210> 21
 <211> 702
 <212> DNA
 <213> Homo Sapien

<220>
 <221> CDS
 <222> (1)...(699)
 <223> Nucleic Acid encoding protease domain of
 endotheliase 1

<400> 21
 agg atc gtt ggt ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag 48
 Arg Ile Val Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15

 gct agc ctg cag tgg gat ggg agt cat cgc tgt gga gca acc tta att 96
 Ala Ser Leu Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile
 20 25 30

 aat gcc aca tgg ctt gtg agt gct gct cac tgt ttt aca aca tat aag 144
 Asn Ala Thr Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys
 35 40 45

 aac cct gcc aga tgg act gct tcc ttt gga gta aca ata aaa cct tcg 192
 Asn Pro Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser
 50 55 60

 aaa atg aaa cgg ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa 240
 Lys Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 65 70 75 80

 cac cca tca cat gac tat gat att tct ctt gca gag ctt tct agc cct 288
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro
 85 90 95

 gtt ccc tac aca aat gca gta cat aga gtt tgt ctc cct gat gca tcc 336
 Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser
 100 105 110

 tat gag ttt caa cca ggt gat gtg atg ttt gtg aca gga ttt gga gca 384
 Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala
 115 120 125

 ctg aaa aat gat ggt tac agt caa aat cat ctt cga caa gca cag gtg 432
 Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val
 130 135 140

 act ctc ata gac gct aca act tgc aat gaa cct caa gct tac aat gac 480
 Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp
 145 150 155 160

-42-

225

230

<210> 23

<211> 1689

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(1689)

<223> Nucleic acid encoding Endotheliase 2-S protein

<400> 23

atg gag agg gac agc cac ggg aat gca tct cca gca aga aca cct tca	48
Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser	
1 5 10 15	
gct gga gca tct cca gcc cag gca tct cca gct ggg aca cct cca ggc	96
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly	
20 25 30	
cgg gca tct cca gcc cag gca tct cca gcc cag gca tct cca gct ggg	144
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly	
35 40 45	
aca cct ccg ggc cgg gca tct cca gcc cag gca tct cca gct ggt aca	192
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr	
50 55 60	
cct cca ggc cgg gca tct cca gcc cgg gca tct cca gcc cag gca tct	240
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser	
65 70 75 80	
cca gcc cgg gca tct ccg gct ctg gca tca ctt tcc agg tcc tca tcc	288
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser	
85 90 95	
ggc agg tca tca tcc gcc agg tca gcc tcg gtg aca acc tcc cca acc	336
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr	
100 105 110	
aga gtg tac ctt gtt aga gca aca cca gtg ggg gct gta ccc atc cga	384
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg	
115 120 125	
tca tct cct gcc agg tca gca cca gca acc agg gcc acc agg gag agc	432
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser	
130 135 140	
cca ggt acg agc ctg ccc aag ttc acc tgg cgg gag ggc cag aag cag	480
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln	
145 150 155 160	
cta ccg ctc atc ggg tgc gtg ctc ctc ctc att gcc ctg gtg gtt tcg	528
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser	
165 170 175	
ctc atc atc ctc ttc cag ttc tgg cag ggc cac aca ggg atc agg tac	576
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr	
180 185 190	

-43-

aag gag cag agg gag agc tgt ccc aag cac gct gtt cgc tgt gac ggg Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly 195 200 205	624
gtg gtg gac tgc aag ctg aag agt gac gag ctg ggc tgc gtg agg ttt Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe 210 215 220	672
gac tgg gac aag tct ctg ctt aaa atc tac tct ggg tcc tcc cat cag Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln 225 230 235 240	720
tgg ctt ccc atc tgt agc agc aac tgg aat gac tcc tac tca gag aag Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys 245 250 255	768
acc tgc cag cag ctg ggt ttc gag agt gct cac cgg aca acc gag gtt Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val 260 265 270	816
gcc cac agg gat ttt gcc aac agc ttc tca atc ttg aga tac aac tcc Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser 275 280 285	864
acc atc cag gaa agc ctc cac agg tct gaa tgc cct tcc cag cgg tat Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr 290 295 300	912
atc tcc ctc cag tgt tcc cac tgc gga ctg agg gcc atg acc ggg cgg Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg 305 310 315 320	960
atc gtg gga ggg gcg ctg gcc tcg gat agc aag tgg cct tgg caa gtg Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val 325 330 335	1008
agt ctg cac ttc ggc acc acc cac atc tgt gga ggc acg ctc att gac Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp 340 345 350	1056
gcc cag tgg gtg ctc act gcc gcc cac tgc ttc ttc gtg acc cgg gag Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu 355 360 365	1104
aag gtc ctg gag ggc tgg aag gtg tac gcg ggc acc agc aac ctg cac Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His 370 375 380	1152
cag ttg cct gag gca gcc tcc att gcc gag atc atc atc aac agc aat Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn 385 390 395 400	1200
tac acc gat gag gag gac gac tat gac atc gcc ctc atg cgg ctg tcc Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser 405 410 415	1248
aag ccc ctg acc ctg tcc gct cac atc cac cct gct tgc ctc ccc atg Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met 420 425 430	1296

-44-

cat gga cag acc ttt agc ctc aat gag acc tgc tgg atc aca ggc ttt	1344
His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe	
435 440 445	
ggc aag acc agg gag aca gat gac aag aca tcc ccc ttc ctc cgg gag	1392
Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu	
450 455 460	
gtg cag gtc aat ctc atc gac ttc aag aaa tgc aat gac tac ttg gtc	1440
Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val	
465 470 475 480	
tat gac agt tac ctt acc cca agg atg atg tgt gct ggg gac ctt cgt	1488
Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg	
485 490 495	
ggg ggc aga gac tcc tgc cag gga gac agc ggg ggg cct ctt gtc tgt	1536
Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys	
500 505 510	
gag cag aac aac cgc tgg tac ctg gca ggt gtc acc agc tgg ggc aca	1584
Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr	
515 520 525	
ggc tgt ggc cag aga aac aaa cct ggt gtg tac acc aaa gtg aca gaa	1632
Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu	
530 535 540	
gtt ctt ccc tgg att tac agc aag atg gag agc gag gtg cga ttc ata	1680
Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Ser Glu Val Arg Phe Ile	
545 550 555 560	
aaa tcc taa	1689
Lys Ser *	

<210> 24

<211> 562

<212> PRT

<213> homo sapien

<220>

<221> protease domain of endotheliase 2

<222> (321)..(562)

<400> 4

Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser	
1 5 10 15	
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly	
20 25 30	
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly	
35 40 45	
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr	
50 55 60	
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser	
65 70 75 80	
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser	
85 90 95	
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr	
100 105 110	
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg	
115 120 125	

-45-

Ser	Ser	Pro	Ala	Arg	Ser	Ala	Pro	Ala	Thr	Arg	Ala	Thr	Arg	Glu	Ser
	130					135					140				
Pro	Gly	Thr	Ser	Leu	Pro	Lys	Phe	Thr	Trp	Arg	Glu	Gly	Gln	Lys	Gln
145					150					155					160
Leu	Pro	Leu	Ile	Gly	Cys	Val	Leu	Leu	Leu	Ile	Ala	Leu	Val	Val	Ser
				165					170						175
Leu	Ile	Ile	Leu	Phe	Gln	Phe	Trp	Gln	Gly	His	Thr	Gly	Ile	Arg	Tyr
			180				185						190		
Lys	Glu	Gln	Arg	Glu	Ser	Cys	Pro	Lys	His	Ala	Val	Arg	Cys	Asp	Gly
		195					200					205			
Val	Val	Asp	Cys	Lys	Leu	Lys	Ser	Asp	Glu	Leu	Gly	Cys	Val	Arg	Phe
	210					215					220				
Asp	Trp	Asp	Lys	Ser	Leu	Leu	Lys	Ile	Tyr	Ser	Gly	Ser	Ser	His	Gln
225					230					235					240
Trp	Leu	Pro	Ile	Cys	Ser	Ser	Asn	Trp	Asn	Asp	Ser	Tyr	Ser	Glu	Lys
				245					250					255	
Thr	Cys	Gln	Gln	Leu	Gly	Phe	Glu	Ser	Ala	His	Arg	Thr	Thr	Glu	Val
			260				265						270		
Ala	His	Arg	Asp	Phe	Ala	Asn	Ser	Phe	Ser	Ile	Leu	Arg	Tyr	Asn	Ser
		275				280						285			
Thr	Ile	Gln	Glu	Ser	Leu	His	Arg	Ser	Glu	Cys	Pro	Ser	Gln	Arg	Tyr
	290					295					300				
Ile	Ser	Leu	Gln	Cys	Ser	His	Cys	Gly	Leu	Arg	Ala	Met	Thr	Gly	Arg
305					310					315					320
Ile	Val	Gly	Gly	Ala	Leu	Ala	Ser	Asp	Ser	Lys	Trp	Pro	Trp	Gln	Val
				325					330					335	
Ser	Leu	His	Phe	Gly	Thr	Thr	His	Ile	Cys	Gly	Gly	Thr	Leu	Ile	Asp
			340					345					350		
Ala	Gln	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Phe	Val	Thr	Arg	Glu
		355				360						365			
Lys	Val	Leu	Glu	Gly	Trp	Lys	Val	Tyr	Ala	Gly	Thr	Ser	Asn	Leu	His
	370					375					380				
Gln	Leu	Pro	Glu	Ala	Ala	Ser	Ile	Ala	Glu	Ile	Ile	Ile	Asn	Ser	Asn
385					390					395					400
Tyr	Thr	Asp	Glu	Glu	Asp	Asp	Tyr	Asp	Ile	Ala	Leu	Met	Arg	Leu	Ser
				405					410					415	
Lys	Pro	Leu	Thr	Leu	Ser	Ala	His	Ile	His	Pro	Ala	Cys	Leu	Pro	Met
			420					425					430		
His	Gly	Gln	Thr	Phe	Ser	Leu	Asn	Glu	Thr	Cys	Trp	Ile	Thr	Gly	Phe
		435					440					445			
Gly	Lys	Thr	Arg	Glu	Thr	Asp	Asp	Lys	Thr	Ser	Pro	Phe	Leu	Arg	Glu
	450					455					460				
Val	Gln	Val	Asn	Leu	Ile	Asp	Phe	Lys	Lys	Cys	Asn	Asp	Tyr	Leu	Val
465					470					475					480
Tyr	Asp	Ser	Tyr	Leu	Thr	Pro	Arg	Met	Met	Cys	Ala	Gly	Asp	Leu	Arg
				485					490					495	
Gly	Gly	Arg	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys
			500					505					510		
Glu	Gln	Asn	Asn	Arg	Trp	Tyr	Leu	Ala	Gly	Val	Thr	Ser	Trp	Gly	Thr
		515					520					525			
Gly	Cys	Gly	Gln	Arg	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Thr	Glu
	530					535					540				
Val	Leu	Pro	Trp	Ile	Tyr	Ser	Lys	Met	Glu	Ser	Glu	Val	Arg	Phe	Ile
545					550					555					560
Lys	Ser														

<210> 25

<211> 2067

<212> DNA

<213> Homo Sapien

-46-

<220>

<221> CDS

<222> (1)...(2067)

<223> Nucleic acid encoding (endotheliase 2-L) protein

<400> 25

atg gag agg gac agc cac ggg aat gca tct cca gca aga aca cct tca	48
Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser	
1 5 10 15	
gct gga gca tct cca gcc cag gca tct cca gct ggg aca cct cca ggc	96
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly	
20 25 30	
cgg gca tct cca gcc cag gca tct cca gcc cag gca tct cca gct ggg	144
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly	
35 40 45	
aca cct ccg ggc cgg gca tct cca gcc cag gca tct cca gct ggt aca	192
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr	
50 55 60	
cct cca ggc cgg gca tct cca ggc cgg gca tct cca gcc cag gca tct	240
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser	
65 70 75 80	
cca gcc cgg gca tct ccg gct ctg gca tca ctt tcc agg tcc tca tcc	288
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser	
85 90 95	
ggc agg tca tca tcc gcc agg tca gcc tcg gtg aca acc tcc cca acc	336
Gly Arg Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr	
100 105 110	
aga gtg tac ctt gtt aga gca aca cca gtg ggg gct gta ccc atc cga	384
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg	
115 120 125	
tca tct cct gcc agg tca gca cca gca acc agg gcc acc agg gag agc	432
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser	
130 135 140	
cca ggt acg agc ctg ccc aag ttc acc tgg cgg gag ggc cag aag cag	480
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln	
145 150 155 160	
cta ccg ctc atc ggg tgc gtg ctc ctc ctc att gcc ctg gtg gtt tcg	528
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser	
165 170 175	
ctc atc atc ctc ttc cag ttc tgg cag ggc cac aca ggg atc agg tac	576
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg Tyr	
180 185 190	
aag gag cag agg gag agc tgt ccc aag cac gct gtt cgc tgt gac ggg	624
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly	
195 200 205	
gtg gtg gac tgc aag ctg aag agt gac gag ctg ggc tgc gtg agg ttt	672
Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe	
210 215 220	

-47-

gac tgg gac aag tct ctg ctt aaa atc tac tct ggg tcc tcc cat cag Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln 225 230 235 240	720
tgg ctt ccc atc tgt agc agc aac tgg aat gac tcc tac tca gag aag Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys 245 250 255	768
acc tgc cag cag ctg ggt ttc gag agt gct cac cgg aca acc gag gtt Thr Cys Gln Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val 260 265 270	816
gcc cac agg gat ttt gcc aac agc ttc tca atc ttg aga tac aac tcc Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser 275 280 285	864
acc atc cag gaa agc ctc cac agg tct gaa tgc cct tcc cag cgg tat Thr Ile Gln Glu Ser Leu His Arg Ser Glu Cys Pro Ser Gln Arg Tyr 290 295 300	912
atc tcc ctc cag tgt tcc cac tgc gga ctg agg gcc atg acc ggg cgg Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg 305 310 315 320	960
atc gtg gga ggg gcg ctg gcc tcg gat agc aag tgg cct tgg caa gtg Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val 325 330 335	1008
agt ctg cac ttc ggc acc acc cac atc tgt gga ggc acg ctc att gac Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp 340 345 350	1056
gcc cag tgg gtg ctc act gcc gcc cac tgc ttc ttc gtg acc cgg gag Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu 355 360 365	1104
aag gtc ctg gag ggc tgg aag gtg tac gcg ggc acc agc aac ctg cac Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His 370 375 380	1152
cag ttg cct gag gca gcc tcc att gcc gag atc atc atc aac agc aat Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn 385 390 395 400	1200
tac acc gat gag gag gac gac tat gac atc gcc ctc atg cgg ctg tcc Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser 405 410 415	1248
aag ccc ctg acc ctg tcc gct cac atc cac cct gct tgc ctc ccc atg Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met 420 425 430	1296
cat gga cag acc ttt agc ctc aat gag acc tgc tgg atc aca ggc ttt His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe 435 440 445	1344
ggc aag acc agg gag aca gat gac aag aca tcc ccc ttc ctc cgg gag Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu 450 455 460	1392

-48-

gtg cag gtc aat ctc atc gac ttc aag aaa tgc aat gac tac ttg gtc Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val 465 470 475 480	1440
tat gac agt tac ctt acc cca agg atg atg tgt gct ggg gac ctt cgt Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg 485 490 495	1488
ggg ggc aga gac tcc tgc cag gga gac agc ggg ggg cct ctt gtc tgt Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys 500 505 510	1536
gag cag aac aac cgc tgg tac ctg gca ggt gtc acc agc tgg ggc aca Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr 515 520 525	1584
ggc tgt ggc cag aga aac aaa cct ggt gtg tac acc aaa gtg aca gaa Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu 530 535 540	1632
gtt ctt ccc tgg att tac agc aag atg gag aac aga gct cag cgg gtt Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Asn Arg Ala Gln Arg Val 545 550 555 560	1680
gaa aaa gcg tgg acc tac agg cca ggc agg cag ttg ctg ggc aga tgt Glu Lys Ala Trp Thr Tyr Arg Pro Gly Arg Gln Leu Leu Gly Arg Cys 565 570 575	1728
tct ccc aga agt att ttt ttg tgt aag gtt gca atg gac ttt gaa aac Ser Pro Arg Ser Ile Phe Leu Cys Lys Val Ala Met Asp Phe Glu Asn 580 585 590	1776
gtt tca gtt tct gca gag gat ttt gtg ata gtt ttt gtt atc aag cat Val Ser Val Ser Ala Glu Asp Phe Val Ile Val Phe Val Ile Lys His 595 600 605	1824
tta tgc atg gga atc cgc tct tca tgg cct ttc cca gct ctg ttt gtt Leu Cys Met Gly Ile Arg Ser Ser Trp Pro Phe Pro Ala Leu Phe Val 610 615 620	1872
tta gtc ttt ttg att ttc ttt ttg ttg ttg ttg tct ttt tta aaa Leu Val Phe Leu Ile Phe Phe Leu Leu Leu Leu Leu Ser Phe Leu Lys 625 630 635 640	1920
aac aca agt gac tcc att ttg act ctg aca act ttc aca gct gtc acc Asn Thr Ser Asp Ser Ile Leu Thr Leu Thr Thr Phe Thr Ala Val Thr 645 650 655	1968
aga atg ctc cct gag aac tac cat tct ttc cct ttc cca ctt aaa ata Arg Met Leu Pro Glu Asn Tyr His Ser Phe Pro Phe Pro Leu Lys Ile 660 665 670	2016
ttt cat cag aac ctc act act atc ata aaa gag tat aaa gta ata aaa Phe His Gln Asn Leu Thr Thr Ile Ile Lys Glu Tyr Lys Val Ile Lys 675 680 685	2064
taa	2067
<210> 26	
<211> 688	
<212> PRT	

-49-

<213> Homo Sapien

<220>

<221> protease domain

<222> (321)..(688)

<400> 26

Met	Glu	Arg	Asp	Ser	His	Gly	Asn	Ala	Ser	Pro	Ala	Arg	Thr	Pro	Ser	1	5	10	15
Ala	Gly	Ala	Ser	Pro	Ala	Gln	Ala	Ser	Pro	Ala	Gly	Thr	Pro	Pro	Gly	20	25	30	
Arg	Ala	Ser	Pro	Ala	Gln	Ala	Ser	Pro	Ala	Gln	Ala	Ser	Pro	Ala	Gly	35	40	45	
Thr	Pro	Pro	Gly	Arg	Ala	Ser	Pro	Ala	Gln	Ala	Ser	Pro	Ala	Gly	Thr	50	55	60	
Pro	Pro	Gly	Arg	Ala	Ser	Pro	Gly	Arg	Ala	Ser	Pro	Ala	Gln	Ala	Ser	65	70	75	80
Pro	Ala	Arg	Ala	Ser	Pro	Ala	Leu	Ala	Ser	Leu	Ser	Arg	Ser	Ser	Ser	85	90	95	
Gly	Arg	Ser	Ser	Ser	Ala	Arg	Ser	Ala	Ser	Val	Thr	Thr	Ser	Pro	Thr	100	105	110	
Arg	Val	Tyr	Leu	Val	Arg	Ala	Thr	Pro	Val	Gly	Ala	Val	Pro	Ile	Arg	115	120	125	
Ser	Ser	Pro	Ala	Arg	Ser	Ala	Pro	Ala	Thr	Arg	Ala	Thr	Arg	Glu	Ser	130	135	140	
Pro	Gly	Thr	Ser	Leu	Pro	Lys	Phe	Thr	Trp	Arg	Glu	Gly	Gln	Lys	Gln	145	150	155	160
Leu	Pro	Leu	Ile	Gly	Cys	Val	Leu	Leu	Leu	Ile	Ala	Leu	Val	Val	Ser	165	170	175	
Leu	Ile	Ile	Leu	Phe	Gln	Phe	Trp	Gln	Gly	His	Thr	Gly	Ile	Arg	Tyr	180	185	190	
Lys	Glu	Gln	Arg	Glu	Ser	Cys	Pro	Lys	His	Ala	Val	Arg	Cys	Asp	Gly	195	200	205	
Val	Val	Asp	Cys	Lys	Leu	Lys	Ser	Asp	Glu	Leu	Gly	Cys	Val	Arg	Phe	210	215	220	
Asp	Trp	Asp	Lys	Ser	Leu	Leu	Lys	Ile	Tyr	Ser	Gly	Ser	Ser	His	Gln	225	230	235	240
Trp	Leu	Pro	Ile	Cys	Ser	Ser	Asn	Trp	Asn	Asp	Ser	Tyr	Ser	Glu	Lys	245	250	255	
Thr	Cys	Gln	Gln	Leu	Gly	Phe	Glu	Ser	Ala	His	Arg	Thr	Thr	Glu	Val	260	265	270	
Ala	His	Arg	Asp	Phe	Ala	Asn	Ser	Phe	Ser	Ile	Leu	Arg	Tyr	Asn	Ser	275	280	285	
Thr	Ile	Gln	Glu	Ser	Leu	His	Arg	Ser	Glu	Cys	Pro	Ser	Gln	Arg	Tyr	290	295	300	
Ile	Ser	Leu	Gln	Cys	Ser	His	Cys	Gly	Leu	Arg	Ala	Met	Thr	Gly	Arg	305	310	315	320
Ile	Val	Gly	Gly	Ala	Leu	Ala	Ser	Asp	Ser	Lys	Trp	Pro	Trp	Gln	Val	325	330	335	
Ser	Leu	His	Phe	Gly	Thr	Thr	His	Ile	Cys	Gly	Gly	Thr	Leu	Ile	Asp	340	345	350	
Ala	Gln	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Phe	Val	Thr	Arg	Glu	355	360	365	
Lys	Val	Leu	Glu	Gly	Trp	Lys	Val	Tyr	Ala	Gly	Thr	Ser	Asn	Leu	His	370	375	380	
Gln	Leu	Pro	Glu	Ala	Ala	Ser	Ile	Ala	Glu	Ile	Ile	Ile	Asn	Ser	Asn	385	390	395	400
Tyr	Thr	Asp	Glu	Glu	Asp	Asp	Tyr	Asp	Ile	Ala	Leu	Met	Arg	Leu	Ser	405	410	415	
Lys	Pro	Leu	Thr	Leu	Ser	Ala	His	Ile	His	Pro	Ala	Cys	Leu	Pro	Met	420	425	430	

-50-

His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
 435 440 445
 Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
 450 455 460
 Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
 465 470 475 480
 Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu Arg
 485 490 495
 Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
 500 505 510
 Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
 515 520 525
 Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
 530 535 540
 Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Asn Arg Ala Gln Arg Val
 545 550 555 560
 Glu Lys Ala Trp Thr Tyr Arg Pro Gly Arg Gln Leu Leu Gly Arg Cys
 565 570 575
 Ser Pro Arg Ser Ile Phe Leu Cys Lys Val Ala Met Asp Phe Glu Asn
 580 585 590
 Val Ser Val Ser Ala Glu Asp Phe Val Ile Val Phe Val Ile Lys His
 595 600 605
 Leu Cys Met Gly Ile Arg Ser Ser Trp Pro Phe Pro Ala Leu Phe Val
 610 615 620
 Leu Val Phe Leu Ile Phe Phe Leu Leu Leu Leu Ser Phe Leu Lys
 625 630 635 640
 Asn Thr Ser Asp Ser Ile Leu Thr Leu Thr Thr Phe Thr Ala Val Thr
 645 650 655
 Arg Met Leu Pro Glu Asn Tyr His Ser Phe Pro Phe Pro Leu Lys Ile
 660 665 670
 Phe His Gln Asn Leu Thr Thr Ile Ile Lys Glu Tyr Lys Val Ile Lys
 675 680 685

<210> 27
 <211> 1471
 <212> DNA
 <213> Homo Sapien

<220>
 <223> DESC1 gene
 <221> misc_feature
 <222> (626)...(1324)
 <223> protease domain

<221> CDS
 <222> (56)...(1324)

<400> 27
 tgacttggat gtagacctcg accttcacag gactcttcat tgctggttgg caatg atg 58
 Met
 1
 tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa ccc 106
 Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu Pro
 5 10 15
 tgg gtt atc ggc ctc gtc ats ttc ata tcc ctg att gtc ctg gca gtg 154
 Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala Val
 20 25 30

-51-

tgc att gga stc act gtt cat tat gtg aga tat aat caa aag aag acc	202
Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys Thr	
35 40 45	
tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat gct	250
Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr Ala	
50 55 60 65	
gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag aga	298
Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln Arg	
70 75 80	
ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg gaa	346
Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg Glu	
85 90 95	
gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat gga	394
Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His Gly	
100 105 110	
gtg ttg gct cat atg ctg ttg att tgt aga ttt cac tct act gag gat	442
Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu Asp	
115 120 125	
cct gaa act gta gat aaa att gtt caa ctt gtt tta cat gaa aag ctg	490
Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys Leu	
130 135 140 145	
caa gat gct gta gga ccc cct aaa gta gat cct cac tca gtt aaa att	538
Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile	
150 155 160	
aaa aaa atc aac aag aca gaa aca gac agc tat cta aac cat tgc tgc	586
Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys	
165 170 175	
gga aca cga aga agt aaa act cta ggt cag agt ctc agg atc gtt ggt	634
Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly	
180 185 190	
ggg aca gaa gta gaa gag ggt gaa tgg ccc tgg cag gct agc ctg cag	682
Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln	
195 200 205	
tgg gat ggg agt cat cgc tgt gga gca acc tta att aat gcc aca tgg	730
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr Trp	
210 215 220 225	
ctt gtg agt gct gct cac tgt ttt aca aca tat aag aac cct gcc aga	778
Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala Arg	
230 235 240	
tgg act gct tcc ttt gga gta aca ata aaa cct tgc aaa atg aaa cgg	826
Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys Arg	
245 250 255	
ggt ctc cgg aga ata att gtc cat gaa aaa tac aaa cac cca tca cat	874
Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser His	
260 265 270	
gac tat gat att tct ctt gca gag ctt tct agc cct gtt ccc tac aca	922

-52-

```

Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr Thr
 275                280                285

aat gca gta cat aga gtt tgt ctc cct gat gca tcc tat gag ttt caa      970
Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe Gln
290                295                300                305

cca ggt gat gtg atg ttt gtg aca gga ttt gga gca ctg aaa aat gat      1018
Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn Asp
                310                315                320

ggt tac agt caa aat cat ctt cga caa gca cag gtg act ctc ata gac      1066
Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile Asp
                325                330                335

gct aca act tgc aat gaa cct caa gct tac aat gac gcc ata act cct      1114
Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr Pro
                340                345                350

aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc cag      1162
Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln
                355                360                365

ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc tgg      1210
Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp
370                375                380                385

tac ctt gct gga ata gtg agc tsg gga gat gaa tgt gcg aaa ccc aac      1258
Tyr Leu Ala Gly Ile Val Ser Xaa Gly Asp Glu Cys Ala Lys Pro Asn
                390                395                400

aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att act      1306
Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr
                405                410                415

tca aaa act ggt atc taa gagagaaaag cctcatggaa cagataacat      1354
Ser Lys Thr Gly Ile *
                420

ttttttttgt tttttgggtg tggaggccat ttttagagat acagaattgg agaagacttg      1414
caaaacagct agatttgact gatctcaata aactgtttgc ttgatgcaaa aaaaaaa      1471

<210> 28
<211> 4933
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (94)...(3222)
<223> Nucleotide sequence encoding corin

<300>
<308> GenBank AF133845
<309> 1999-05-24

<400> 28
aatcatccg tagtgctcc ccgggggaca cgtagaggag agaaaagcga ccaagataaa      60
agtggacaga agaataagcg agacttttta tcc atg aaa cag tct cct gcc ctc      114
Met Lys Gln Ser Pro Ala Leu
                1                5

```

-53-

gct cgc gaa gag cgc tac cgc aga gcc ggg tcc cca aag ccg gtc ttg	162
Ala Pro Glu Glu Arg Tyr Arg Arg Ala Gly Ser Pro Lys Pro Val Leu	
10 15 20	
aga gct gat gac aat aac atg ggc aat ggc tgc tct cag aag ctg gcg	210
Arg Ala Asp Asp Asn Asn Met Gly Asn Gly Cys Ser Gln Lys Leu Ala	
25 30 35	
act gct aac ctc ctc cgg ttc cta ttg ctg gtc ctg att cca tgt atc	258
Thr Ala Asn Leu Leu Arg Phe Leu Leu Leu Val Leu Ile Pro Cys Ile	
40 45 50 55	
tgt gct ctc gtt ctc ttg ctg gtg atc ctg ctt tcc tat gtt gga aca	306
Cys Ala Leu Val Leu Leu Leu Val Ile Leu Leu Ser Tyr Val Gly Thr	
60 65 70	
tta caa aag gtc tat ttt aaa tca aat ggg agt gaa cct ttg gtc act	354
Leu Gln Lys Val Tyr Phe Lys Ser Asn Gly Ser Glu Pro Leu Val Thr	
75 80 85	
gat ggt gaa atc caa ggg tcc gat gtt att ctt aca aat aca att tat	402
Asp Gly Glu Ile Gln Gly Ser Asp Val Ile Leu Thr Asn Thr Ile Tyr	
90 95 100	
aac cag agc act gtg gtg tct act gca cat ccc gac caa cac gtt cca	450
Asn Gln Ser Thr Val Val Ser Thr Ala His Pro Asp Gln His Val Pro	
105 110 115	
gcc tgg act acg gat gct tct ctc cca ggg gac caa agt cac agg aat	498
Ala Trp Thr Thr Asp Ala Ser Leu Pro Gly Asp Gln Ser His Arg Asn	
120 125 130 135	
aca agt gcc tgt atg aac atc acc cac agc cag tgt cag atg ctg ccc	546
Thr Ser Ala Cys Met Asn Ile Thr His Ser Gln Cys Gln Met Leu Pro	
140 145 150	
tac cac gcc acg ctg aca cct ctc ctc tca gtt gtc aga aac atg gaa	594
Tyr His Ala Thr Leu Thr Pro Leu Leu Ser Val Val Arg Asn Met Glu	
155 160 165	
atg gaa aag ttc ctc aag ttt ttc aca tat ctc cat cgc ctc agt tgc	642
Met Glu Lys Phe Leu Lys Phe Phe Thr Tyr Leu His Arg Leu Ser Cys	
170 175 180	
tat caa cat atc atg ctg ttt ggc tgt acc ctc gcc ttc cct gag tgc	690
Tyr Gln His Ile Met Leu Phe Gly Cys Thr Leu Ala Phe Pro Glu Cys	
185 190 195	
atc att gat ggc gat gac agt cat gga ctc ctg ccc tgt agg tcc ttc	738
Ile Ile Asp Gly Asp Asp Ser His Gly Leu Leu Pro Cys Arg Ser Phe	
200 205 210 215	
tgt gag gct gca aaa gaa ggc tgt gaa tca gtc ctg ggg atg gtg aat	786
Cys Glu Ala Ala Lys Glu Gly Cys Glu Ser Val Leu Gly Met Val Asn	
220 225 230	
tac tcc tgg ccg gat ttc ctc aga tgc tcc cag ttt aga aac caa act	834
Tyr Ser Trp Pro Asp Phe Leu Arg Cys Ser Gln Phe Arg Asn Gln Thr	
235 240 245	

-54-

gaa agc agc aat gtc agc aga att tgc ttc tca cct cag cag gaa aac	882
Glu Ser Ser Asn Val Ser Arg Ile Cys Phe Ser Pro Gln Gln Glu Asn	
250 255 260	
gga aag caa ttg ctc tgt gga agg ggt gag aac ttt ctg tgt gcc agt	930
Gly Lys Gln Leu Leu Cys Gly Arg Gly Glu Asn Phe Leu Cys Ala Ser	
265 270 275	
gga atc tgc atc ccc ggg aaa ctg caa tgt aat ggc tac aac gac tgt	978
Gly Ile Cys Ile Pro Gly Lys Leu Gln Cys Asn Gly Tyr Asn Asp Cys	
280 285 290 295	
gac gac tgg agt gac gag gct cat tgc aac tgc agc gag aat ctg ttt	1026
Asp Asp Trp Ser Asp Glu Ala His Cys Asn Cys Ser Glu Asn Leu Phe	
300 305 310	
cac tgt cac aca ggc aag tgc ctt aat tac agc ctt gtg tgt gat gga	1074
His Cys His Thr Gly Lys Cys Leu Asn Tyr Ser Leu Val Cys Asp Gly	
315 320 325	
tat gat gac tgt ggg gat ttg agt gat gag caa aac tgt gat tgc aat	1122
Tyr Asp Asp Cys Gly Asp Leu Ser Asp Glu Gln Asn Cys Asp Cys Asn	
330 335 340	
ccc aca aca gag cat cgc tgc ggg gac ggg cgc tgc atc gcc atg gag	1170
Pro Thr Thr Glu His Arg Cys Gly Asp Gly Arg Cys Ile Ala Met Glu	
345 350 355	
tgg gtg tgt gat ggt gac cac gac tgt gtg gat aag tcc gac gag gtc	1218
Trp Val Cys Asp Gly Asp His Asp Cys Val Asp Lys Ser Asp Glu Val	
360 365 370 375	
aac tgc tcc tgt cac agc cag ggt ctg gtg gaa tgc aga aat gga caa	1266
Asn Cys Ser Cys His Ser Gln Gly Leu Val Glu Cys Arg Asn Gly Gln	
380 385 390	
tgt atc ccc agc acg ttt caa tgt gat ggt gac gag gac tgc aag gat	1314
Cys Ile Pro Ser Thr Phe Gln Cys Asp Gly Asp Glu Asp Cys Lys Asp	
395 400 405	
ggg agt gat gag gag aac tgc agc gtc att cag act tca tgt caa gaa	1362
Gly Ser Asp Glu Glu Asn Cys Ser Val Ile Gln Thr Ser Cys Gln Glu	
410 415 420	
gga gac caa aga tgc ctc tac aat ccc tgc ctt gat tca tgt ggt ggt	1410
Gly Asp Gln Arg Cys Leu Tyr Asn Pro Cys Leu Asp Ser Cys Gly Gly	
425 430 435	
agc tct ctc tgt gac ccg aac aac agt ctg aat aac tgt agt caa tgt	1458
Ser Ser Leu Cys Asp Pro Asn Asn Ser Leu Asn Asn Cys Ser Gln Cys	
440 445 450 455	
gaa cca att aca ttg gaa ctc tgc atg aat ttg ccc tac aac agt aca	1506
Glu Pro Ile Thr Leu Glu Leu Cys Met Asn Leu Pro Tyr Asn Ser Thr	
460 465 470	
agt tat cca aat tat ttt ggc cac agg act caa aag gaa gca tcc atc	1554
Ser Tyr Pro Asn Tyr Phe Gly His Arg Thr Gln Lys Glu Ala Ser Ile	
475 480 485	
agc tgg gag tct tct ctt ttc cct gca ctt gtt caa acc aac tgt tat	1602

-55-

Ser	Trp	Glu	Ser	Ser	Leu	Phe	Pro	Ala	Leu	Val	Gln	Thr	Asn	Cys	Tyr	
		490					495					500				
aaa	tac	ctc	atg	ttc	ttt	tct	tgc	acc	att	ttg	gta	cca	aaa	tgt	gat	1650
Lys	Tyr	Leu	Met	Phe	Phe	Ser	Cys	Thr	Ile	Leu	Val	Pro	Lys	Cys	Asp	
	505					510					515					
gtg	aat	aca	ggc	gag	cgt	atc	cct	cct	tgc	agg	gca	ttg	tgt	gaa	cac	1698
Val	Asn	Thr	Gly	Glu	Arg	Ile	Pro	Pro	Cys	Arg	Ala	Leu	Cys	Glu	His	
520					525					530					535	
tct	aaa	gaa	cgc	tgt	gag	tct	gtt	ctt	ggg	att	gtg	ggc	cta	cag	tgg	1746
Ser	Lys	Glu	Arg	Cys	Glu	Ser	Val	Leu	Gly	Ile	Val	Gly	Leu	Gln	Trp	
				540					545					550		
cct	gaa	gac	aca	gat	tgc	agt	caa	ttt	cca	gag	gaa	aat	tca	gac	aat	1794
Pro	Glu	Asp	Thr	Asp	Cys	Ser	Gln	Phe	Pro	Glu	Glu	Asn	Ser	Asp	Asn	
			555					560					565			
caa	acc	tgc	ctg	atg	cct	gat	gaa	tat	gtg	gaa	gaa	tgc	tca	cct	agt	1842
Gln	Thr	Cys	Leu	Met	Pro	Asp	Glu	Tyr	Val	Glu	Glu	Cys	Ser	Pro	Ser	
		570					575					580				
cat	ttc	aag	tgc	cgc	tca	gga	cag	tgt	gtt	ctg	gct	tcc	aga	aga	tgt	1890
His	Phe	Lys	Cys	Arg	Ser	Gly	Gln	Cys	Val	Leu	Ala	Ser	Arg	Arg	Cys	
	585					590					595					
gat	ggc	cag	gcc	gac	tgt	gac	gat	gac	agt	gat	gag	gaa	aac	tgt	ggc	1938
Asp	Gly	Gln	Ala	Asp	Cys	Asp	Asp	Asp	Ser	Asp	Glu	Glu	Asn	Cys	Gly	
600					605					610					615	
tgt	aaa	gag	aga	gat	ctt	tgg	gaa	tgt	cca	tcc	aat	aaa	caa	tgt	ttg	1986
Cys	Lys	Glu	Arg	Asp	Leu	Trp	Glu	Cys	Pro	Ser	Asn	Lys	Gln	Cys	Leu	
				620					625					630		
aag	cac	aca	gtg	atc	tgc	gat	ggg	ttc	cca	gac	tgc	cct	gat	tac	atg	2034
Lys	His	Thr	Val	Ile	Cys	Asp	Gly	Phe	Pro	Asp	Cys	Pro	Asp	Tyr	Met	
			635					640					645			
gac	gag	aaa	aac	tgc	tca	ttt	tgc	caa	gat	gat	gag	ctg	gaa	tgt	gca	2082
Asp	Glu	Lys	Asn	Cys	Ser	Phe	Cys	Gln	Asp	Asp	Glu	Leu	Glu	Cys	Ala	
		650					655					660				
aac	cat	gcg	tgt	gtg	tca	cgt	gac	ctg	tgg	tgt	gat	ggc	gaa	gcc	gac	2130
Asn	His	Ala	Cys	Val	Ser	Arg	Asp	Leu	Trp	Cys	Asp	Gly	Glu	Ala	Asp	
	665					670					675					
tgc	tca	gac	agt	tca	gat	gaa	tgg	gac	tgt	gtg	acc	ctc	tct	ata	aat	2178
Cys	Ser	Asp	Ser	Ser	Asp	Glu	Trp	Asp	Cys	Val	Thr	Leu	Ser	Ile	Asn	
680					685					690					695	
gtg	aac	tcc	tct	tcc	ttt	ctg	atg	gtt	cac	aga	gct	gcc	aca	gaa	cac	2226
Val	Asn	Ser	Ser	Ser	Phe	Leu	Met	Val	His	Arg	Ala	Ala	Thr	Glu	His	
				700					705					710		
cat	gtg	tgt	gca	gat	ggc	tgg	cag	gag	ata	ttg	agt	cag	ctg	gcc	tgc	2274
His	Val	Cys	Ala	Asp	Gly	Trp	Gln	Glu	Ile	Leu	Ser	Gln	Leu	Ala	Cys	
			715				720						725			
aag	cag	atg	ggc	tta	gga	gaa	cca	tct	gtg	acc	aaa	ttg	ata	cag	gaa	2322
Lys	Gln	Met	Gly	Leu	Gly	Glu	Pro	Ser	Val	Thr	Lys	Leu	Ile	Gln	Glu	

-56-

730					735					740						
cag	gag	aaa	gag	ccg	cgg	tgg	ctg	aca	tta	cac	tcc	aac	tgg	gag	agc	2370
Gln	Glu	Lys	Glu	Pro	Arg	Trp	Leu	Thr	Leu	His	Ser	Asn	Trp	Glu	Ser	
	745					750					755					
ctc	aat	ggg	acc	act	tta	cat	gaa	ctt	cta	gta	aat	ggg	cag	tct	tgt	2418
Leu	Asn	Gly	Thr	Thr	Leu	His	Glu	Leu	Leu	Val	Asn	Gly	Gln	Ser	Cys	
	760				765				770						775	
gag	agc	aga	agt	aaa	att	tct	ctt	ctg	tgt	act	aaa	caa	gac	tgt	ggg	2466
Glu	Ser	Arg	Ser	Lys	Ile	Ser	Leu	Leu	Cys	Thr	Lys	Gln	Asp	Cys	Gly	
				780				785						790		
cgc	cgc	cct	gct	gcc	cga	atg	aac	aaa	agg	atc	ctt	gga	ggt	cgg	acg	2514
Arg	Arg	Pro	Ala	Ala	Arg	Met	Asn	Lys	Arg	Ile	Leu	Gly	Gly	Arg	Thr	
			795					800					805			
agt	cgc	cct	gga	agg	tgg	cca	tgg	cag	tgt	tct	ctg	cag	agt	gaa	ccc	2562
Ser	Arg	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Cys	Ser	Leu	Gln	Ser	Glu	Pro	
		810					815					820				
agt	gga	cat	atc	tgt	ggc	tgt	gtc	ctc	att	gcc	aag	aag	tgg	gtt	ctg	2610
Ser	Gly	His	Ile	Cys	Gly	Cys	Val	Leu	Ile	Ala	Lys	Lys	Trp	Val	Leu	
	825					830					835					
aca	gtt	gcc	cac	tgc	ttc	gag	ggg	aga	gag	aat	gct	gca	gtt	tgg	aaa	2658
Thr	Val	Ala	His	Cys	Phe	Glu	Gly	Arg	Glu	Asn	Ala	Ala	Val	Trp	Lys	
	840				845					850					855	
gtg	gtg	ctt	ggc	atc	aac	aat	cta	gac	cat	cca	tca	gtg	ttc	atg	cag	2706
Val	Val	Leu	Gly	Ile	Asn	Asn	Leu	Asp	His	Pro	Ser	Val	Phe	Met	Gln	
				860					865					870		
aca	cgc	ttt	gtg	aag	acc	atc	atc	ctg	cat	ccc	cgc	tac	agt	cga	gca	2754
Thr	Arg	Phe	Val	Lys	Thr	Ile	Ile	Leu	His	Pro	Arg	Tyr	Ser	Arg	Ala	
			875					880					885			
gtg	gtg	gac	tat	gac	atc	agc	atc	gtt	gag	ctg	agt	gaa	gac	atc	agt	2802
Val	Val	Asp	Tyr	Asp	Ile	Ser	Ile	Val	Glu	Leu	Ser	Glu	Asp	Ile	Ser	
		890				895						900				
gag	act	ggc	tac	gtc	cgg	cct	gtc	tgc	ttg	ccc	aac	ccg	gag	cag	tgg	2850
Glu	Thr	Gly	Tyr	Val	Arg	Pro	Val	Cys	Leu	Pro	Asn	Pro	Glu	Gln	Trp	
	905					910					915					
cta	gag	cct	gac	acg	tac	tgc	tat	atc	aca	ggc	tgg	ggc	cac	atg	ggc	2898
Leu	Glu	Pro	Asp	Thr	Tyr	Cys	Tyr	Ile	Thr	Gly	Trp	Gly	His	Met	Gly	
	920				925					930					935	
aat	aaa	atg	cca	ttt	aag	ctg	caa	gag	gga	gag	gtc	cgc	att	att	tct	2946
Asn	Lys	Met	Pro	Phe	Lys	Leu	Gln	Glu	Gly	Glu	Val	Arg	Ile	Ile	Ser	
				940				945						950		
ctg	gaa	cat	tgt	cag	tcc	tac	ttt	gac	atg	aag	acc	atc	acc	act	cgg	2994
Leu	Glu	His	Cys	Gln	Ser	Tyr	Phe	Asp	Met	Lys	Thr	Ile	Thr	Thr	Arg	
			955					960					965			
atg	ata	tgt	gct	ggc	tat	gag	tct	ggc	aca	gtt	gat	tca	tgc	atg	ggt	3042
Met	Ile	Cys	Ala	Gly	Tyr	Glu	Ser	Gly	Thr	Val	Asp	Ser	Cys	Met	Gly	
		970				975						980				

-57-

gac agc ggt ggg cct ctt gtt tgt gag aag cct gga gga cgg tgg aca 3090
 Asp Ser Gly Gly Pro Leu Val Cys Glu Lys Pro Gly Gly Arg Trp Thr
 985 990 995

tta ttt gga tta act tca tgg ggc tcc gtc tgc ttt tcc aaa gtc ctg 3138
 Leu Phe Gly Leu Thr Ser Trp Gly Ser Val Cys Phe Ser Lys Val Leu
 1000 1005 1010 1015

ggg cct ggc gtt tat agt aat gtg tca tat ttc gtc gaa tgg att aaa 3186
 Gly Pro Gly Val Tyr Ser Asn Val Ser Tyr Phe Val Glu Trp Ile Lys
 1020 1025 1030

aga cag att tac atc cag acc ttt ctc cta aac taa ttataaggat 3232
 Arg Gln Ile Tyr Ile Gln Thr Phe Leu Leu Asn *
 1035 1040

gatcagagac ttttgccagc tacactaaaa gaaaatggcc ttcttgactg tgaagagctg 3292
 cctgcagaga gctgtacaga agcacttttc atggacagaa atgctcaatc gtgcactgca 3352
 aatttgcatg tttgttttgg actaattttt ttcaatttat tttttcacct tcatttttct 3412
 cttattttcaa gttcaatgaa agactttaca aaagcaaaca aagcagactt tgtccttttg 3472
 ccaggcctaa ccatgactgc agcacaaaat tatcgactct ggcgagattt aaaatcaggt 3532
 gctacagtaa caggttatgg aatgggtctct tttatcctat cacaaaaaaa gacatagata 3592
 tttaggctga ttaattatct ctaccagttt ttgtttctca agctcagtgc atagtggtaa 3652
 atttcagtgt taacattgga gacttgcttt tctttttctt tttttatacc ccacaattct 3712
 tttttattac acttcgaatt ttaggggtaca cgagcacaaac gtgcagggtta gttacatatg 3772
 tatacatgtg ccatgttggg gtgctgaacc cagtaactcg tcatttgatt tattaaaagc 3832
 caagataatt tacatgttta aagtatttac tattaccocc ttctaattgt tgcataattc 3892
 tgagaactga taaaagacag caataaaaga ccagtgtcat ccatttaggt agcaagacat 3952
 attgaatgca aagttcttta gatatacaata ttaacacttg acattattgg accccccatt 4012
 ctggatgtat atcaagatca taattttata gaagagtctc tatagaactg tcctcatagc 4072
 tgggtttgtt caggatatat gagttggctg attgagactg caacaactac atctatatat 4132
 atgggcaata ttttgtttta cttatgtggc aaagaactgg atattaaact ttgcaaaaga 4192
 gaatttagat gagagatgca atttttttaa aagaaaatta atttgcatcc ctcgtttaat 4252
 taaatttatt tttcagtttt cttgcgttca tccataccaa caaagtcata aagagcatat 4312
 ttttagagcag agtaagactt tgcattggag aaaacatttt gtaattttcc tcaaaagatg 4372
 tttaatatct ggtttcttct cattggtaat taaaatttta gaaatgattt ttagctctag 4432
 gccactttac gcaactcaat ttctgaagca attagtggta aaaagtattt tccccacta 4492
 aaaaacttta aaacacaaat cttcatatat acttaattta attagtcagg catccatttt 4552
 gcctttttaa caactaggat tccctactaa cctccaccag caacctggac tgcctcagca 4612
 ttccaaatag atactacctg caattttata catgtatttt tgtatctttt ctgtgtgtaa 4672
 acatagttga aattcaaaaa gttgtagcaa tttctatact attcatctcc tgtccttcag 4732
 tttgtataaa cctaaggaga gtgtgaaatc cagcaactga attgtgggtca cgattgtatg 4792
 aaagttcaag aacatatgtc agttttgtta cagttgtagc tacatactca atgtatcaac 4852
 ttttagcctg ctcaacttag gctcagtga atatatatat tatacttatt ttaaataatt 4912
 cttataacaa ataaaatggg a 4933

<210> 29
 <211> 1042
 <212> PRT
 <213> Homo Sapien

<400> 29
 Met Lys Gln Ser Pro Ala Leu Ala Pro Glu Glu Arg Tyr Arg Arg Ala
 1 5 10 15
 Gly Ser Pro Lys Pro Val Leu Arg Ala Asp Asp Asn Asn Met Gly Asn
 20 25 30
 Gly Cys Ser Gln Lys Leu Ala Thr Ala Asn Leu Leu Arg Phe Leu Leu
 35 40 45
 Leu Val Leu Ile Pro Cys Ile Cys Ala Leu Val Leu Leu Leu Val Ile
 50 55 60

-58-

Leu	Leu	Ser	Tyr	Val	Gly	Thr	Leu	Gln	Lys	Val	Tyr	Phe	Lys	Ser	Asn
65					70					75					80
Gly	Ser	Glu	Pro	Leu	Val	Thr	Asp	Gly	Glu	Ile	Gln	Gly	Ser	Asp	Val
				85					90					95	
Ile	Leu	Thr	Asn	Thr	Ile	Tyr	Asn	Gln	Ser	Thr	Val	Val	Ser	Thr	Ala
			100					105					110		
His	Pro	Asp	Gln	His	Val	Pro	Ala	Trp	Thr	Thr	Asp	Ala	Ser	Leu	Pro
		115					120					125			
Gly	Asp	Gln	Ser	His	Arg	Asn	Thr	Ser	Ala	Cys	Met	Asn	Ile	Thr	His
	130					135					140				
Ser	Gln	Cys	Gln	Met	Leu	Pro	Tyr	His	Ala	Thr	Leu	Thr	Pro	Leu	Leu
145					150					155					160
Ser	Val	Val	Arg	Asn	Met	Glu	Met	Glu	Lys	Phe	Leu	Lys	Phe	Phe	Thr
				165					170					175	
Tyr	Leu	His	Arg	Leu	Ser	Cys	Tyr	Gln	His	Ile	Met	Leu	Phe	Gly	Cys
			180					185					190		
Thr	Leu	Ala	Phe	Pro	Glu	Cys	Ile	Ile	Asp	Gly	Asp	Asp	Ser	His	Gly
		195					200					205			
Leu	Leu	Pro	Cys	Arg	Ser	Phe	Cys	Glu	Ala	Ala	Lys	Glu	Gly	Cys	Glu
	210					215					220				
Ser	Val	Leu	Gly	Met	Val	Asn	Tyr	Ser	Trp	Pro	Asp	Phe	Leu	Arg	Cys
225					230					235					240
Ser	Gln	Phe	Arg	Asn	Gln	Thr	Glu	Ser	Ser	Asn	Val	Ser	Arg	Ile	Cys
				245						250				255	
Phe	Ser	Pro	Gln	Gln	Glu	Asn	Gly	Lys	Gln	Leu	Leu	Cys	Gly	Arg	Gly
			260					265					270		
Glu	Asn	Phe	Leu	Cys	Ala	Ser	Gly	Ile	Cys	Ile	Pro	Gly	Lys	Leu	Gln
		275					280					285			
Cys	Asn	Gly	Tyr	Asn	Asp	Cys	Asp	Asp	Trp	Ser	Asp	Glu	Ala	His	Cys
	290					295					300				
Asn	Cys	Ser	Glu	Asn	Leu	Phe	His	Cys	His	Thr	Gly	Lys	Cys	Leu	Asn
305					310					315					320
Tyr	Ser	Leu	Val	Cys	Asp	Gly	Tyr	Asp	Asp	Cys	Gly	Asp	Leu	Ser	Asp
				325					330					335	
Glu	Gln	Asn	Cys	Asp	Cys	Asn	Pro	Thr	Thr	Glu	His	Arg	Cys	Gly	Asp
			340					345					350		
Gly	Arg	Cys	Ile	Ala	Met	Glu	Trp	Val	Cys	Asp	Gly	Asp	His	Asp	Cys
		355					360					365			
Val	Asp	Lys	Ser	Asp	Glu	Val	Asn	Cys	Ser	Cys	His	Ser	Gln	Gly	Leu
	370					375					380				
Val	Glu	Cys	Arg	Asn	Gly	Gln	Cys	Ile	Pro	Ser	Thr	Phe	Gln	Cys	Asp
385					390					395					400
Gly	Asp	Glu	Asp	Cys	Lys	Asp	Gly	Ser	Asp	Glu	Glu	Asn	Cys	Ser	Val
				405					410					415	
Ile	Gln	Thr	Ser	Cys	Gln	Glu	Gly	Asp	Gln	Arg	Cys	Leu	Tyr	Asn	Pro
			420					425					430		
Cys	Leu	Asp	Ser	Cys	Gly	Gly	Ser	Ser	Leu	Cys	Asp	Pro	Asn	Asn	Ser
		435					440					445			
Leu	Asn	Asn	Cys	Ser	Gln	Cys	Glu	Pro	Ile	Thr	Leu	Glu	Leu	Cys	Met
	450					455					460				
Asn	Leu	Pro	Tyr	Asn	Ser	Thr	Ser	Tyr	Pro	Asn	Tyr	Phe	Gly	His	Arg
465					470					475					480
Thr	Gln	Lys	Glu	Ala	Ser	Ile	Ser	Trp	Glu	Ser	Ser	Leu	Phe	Pro	Ala
				485					490					495	
Leu	Val	Gln	Thr	Asn	Cys	Tyr	Lys	Tyr	Leu	Met	Phe	Phe	Ser	Cys	Thr
			500					505					510		
Ile	Leu	Val	Pro	Lys	Cys	Asp	Val	Asn	Thr	Gly	Glu	Arg	Ile	Pro	Pro
		515					520					525			
Cys	Arg	Ala	Leu	Cys	Glu	His	Ser	Lys	Glu	Arg	Cys	Glu	Ser	Val	Leu
	530					535					540				
Gly	Ile	Val	Gly	Leu	Gln	Trp	Pro	Glu	Asp	Thr	Asp	Cys	Ser	Gln	Phe

-59-

545					550					555					560
Pro	Glu	Glu	Asn	Ser	Asp	Asn	Gln	Thr	Cys	Leu	Met	Pro	Asp	Glu	Tyr
				565					570					575	
Val	Glu	Glu	Cys	Ser	Pro	Ser	His	Phe	Lys	Cys	Arg	Ser	Gly	Gln	Cys
			580					585					590		
Val	Leu	Ala	Ser	Arg	Arg	Cys	Asp	Gly	Gln	Ala	Asp	Cys	Asp	Asp	Asp
		595					600				605				
Ser	Asp	Glu	Glu	Asn	Cys	Gly	Cys	Lys	Glu	Arg	Asp	Leu	Trp	Glu	Cys
	610					615					620				
Pro	Ser	Asn	Lys	Gln	Cys	Leu	Lys	His	Thr	Val	Ile	Cys	Asp	Gly	Phe
625					630					635					640
Pro	Asp	Cys	Pro	Asp	Tyr	Met	Asp	Glu	Lys	Asn	Cys	Ser	Phe	Cys	Gln
				645					650					655	
Asp	Asp	Glu	Leu	Glu	Cys	Ala	Asn	His	Ala	Cys	Val	Ser	Arg	Asp	Leu
			660					665					670		
Trp	Cys	Asp	Gly	Glu	Ala	Asp	Cys	Ser	Asp	Ser	Ser	Asp	Glu	Trp	Asp
		675					680					685			
Cys	Val	Thr	Leu	Ser	Ile	Asn	Val	Asn	Ser	Ser	Ser	Phe	Leu	Met	Val
	690					695					700				
His	Arg	Ala	Ala	Thr	Glu	His	His	Val	Cys	Ala	Asp	Gly	Trp	Gln	Glu
705					710					715					720
Ile	Leu	Ser	Gln	Leu	Ala	Cys	Lys	Gln	Met	Gly	Leu	Gly	Glu	Pro	Ser
			725						730					735	
Val	Thr	Lys	Leu	Ile	Gln	Glu	Gln	Glu	Lys	Glu	Pro	Arg	Trp	Leu	Thr
			740					745					750		
Leu	His	Ser	Asn	Trp	Glu	Ser	Leu	Asn	Gly	Thr	Thr	Leu	His	Glu	Leu
	755						760					765			
Leu	Val	Asn	Gly	Gln	Ser	Cys	Glu	Ser	Arg	Ser	Lys	Ile	Ser	Leu	Leu
	770					775					780				
Cys	Thr	Lys	Gln	Asp	Cys	Gly	Arg	Arg	Pro	Ala	Arg	Met	Asn	Lys	
785					790				795					800	
Arg	Ile	Leu	Gly	Gly	Arg	Thr	Ser	Arg	Pro	Gly	Arg	Trp	Pro	Trp	Gln
			805						810					815	
Cys	Ser	Leu	Gln	Ser	Glu	Pro	Ser	Gly	His	Ile	Cys	Gly	Cys	Val	Leu
			820					825				830			
Ile	Ala	Lys	Lys	Trp	Val	Leu	Thr	Val	Ala	His	Cys	Phe	Glu	Gly	Arg
	835						840					845			
Glu	Asn	Ala	Ala	Val	Trp	Lys	Val	Val	Leu	Gly	Ile	Asn	Asn	Leu	Asp
	850					855					860				
His	Pro	Ser	Val	Phe	Met	Gln	Thr	Arg	Phe	Val	Lys	Thr	Ile	Ile	Leu
865					870					875					880
His	Pro	Arg	Tyr	Ser	Arg	Ala	Val	Val	Asp	Tyr	Asp	Ile	Ser	Ile	Val
				885					890					895	
Glu	Leu	Ser	Glu	Asp	Ile	Ser	Glu	Thr	Gly	Tyr	Val	Arg	Pro	Val	Cys
			900					905					910		
Leu	Pro	Asn	Pro	Glu	Gln	Trp	Leu	Glu	Pro	Asp	Thr	Tyr	Cys	Tyr	Ile
		915					920					925			
Thr	Gly	Trp	Gly	His	Met	Gly	Asn	Lys	Met	Pro	Phe	Lys	Leu	Gln	Glu
	930					935					940				
Gly	Glu	Val	Arg	Ile	Ile	Ser	Leu	Glu	His	Cys	Gln	Ser	Tyr	Phe	Asp
945					950					955					960
Met	Lys	Thr	Ile	Thr	Thr	Arg	Met	Ile	Cys	Ala	Gly	Tyr	Glu	Ser	Gly
			965						970					975	
Thr	Val	Asp	Ser	Cys	Met	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Glu
			980				985						990		
Lys	Pro	Gly	Gly	Arg	Trp	Thr	Leu	Phe	Gly	Leu	Thr	Ser	Trp	Gly	Ser
		995					1000					1005			
Val	Cys	Phe	Ser	Lys	Val	Leu	Gly	Pro	Gly	Val	Tyr	Ser	Asn	Val	Ser
	1010					1015					1020				
Tyr	Phe	Val	Glu	Trp	Ile	Lys	Arg	Gln	Ile	Tyr	Ile	Gln	Thr	Phe	Leu
1025					1030					1035					1040

<400> 30																
accagacagt tcttaaatta gcaagccttc aaaaccaaaa atg ggg tcg aaa aga																55
Met Gly Ser Lys Arg																
1 5																
ggc ata tct tct agg cat cat tct ctc agc tcc tat gaa atc atg ttt																103
Gly Ile Ser Ser Arg His His Ser Leu Ser Ser Tyr Glu Ile Met Phe																
10 15 20																
gca gct ctc ttt gcc ata ttg gta gtg ctc tgt gct gga tta att gca																151
Ala Ala Leu Phe Ala Ile Leu Val Val Leu Cys Ala Gly Leu Ile Ala																
25 30 35																
gta tcc tgc ctg aca atc aag gaa tcc caa cga ggt gca gca ctt gga																199
Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg Gly Ala Ala Leu Gly																
40 45 50																
cag agt cat gaa gcc aga gcg aca ttt aaa ata aca tcc gga gtt aca																247
Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile Thr Ser Gly Val Thr																
55 60 65																
tat aat cct aat ttg caa gac aaa ctc tca gtg gat ttc aaa gtt ctt																295
Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val Asp Phe Lys Val Leu																
70 75 80 85																
gct ttt gac ctt cag caa atg ata gat gag atc ttt cta tca agc aat																343
Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile Phe Leu Ser Ser Asn																
90 95 100																
ctg aag aat gaa tat aag aac tca aga gtt tta caa ttt gaa aat ggc																391
Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu Gln Phe Glu Asn Gly																
105 110 115																
agc att ata gtc gta ttt gac ctt ttc ttt gcc cag tgg gtg tca gat																439
Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala Gln Trp Val Ser Asp																
120 125 130																
caa aat gta aaa gaa gaa ctg att caa ggc ctt gaa gca aat aaa tcc																487
Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu Glu Ala Asn Lys Ser																
135 140 145																
agc caa ctg gtc act ttc cat att gat ttg aac agc gtt gat atc cta																535
Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn Ser Val Asp Ile Leu																
150 155 160 165																

-61-

gac aag cta aca acc acc agt cat ctg gca act cca gga aat gtc tca Asp Lys Leu Thr Thr Thr Ser His Leu Ala Thr Pro Gly Asn Val Ser 170 175 180	583
ata gag tgc ctg cct ggt tca agt cct tgt act gat gct cta acg tgt Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr Asp Ala Leu Thr Cys 185 190 195	631
ata aaa gct gat tta ttt tgt gat gga gaa gta aac tgt cca gat ggt Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val Asn Cys Pro Asp Gly 200 205 210	679
tct gac gaa gac aat aaa atg tgt gcc aca gtt tgt gat gga aga ttt Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val Cys Asp Gly Arg Phe 215 220 225	727
ttg tta act gga tca tct ggg tct ttc cag gct act cat tat cca aaa Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala Thr His Tyr Pro Lys 230 235 240 245	775
cct tct gaa aca agt gtt gtc tgc cag tgg atc ata cgt gta aac caa Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile Ile Arg Val Asn Gln 250 255 260	823
gga ctt tcc att aaa ctg agc ttc gat gat ttt aat aca tat tat aca Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe Asn Thr Tyr Tyr Thr 265 270 275	871
gat ata tta gat att tat gaa ggt gta gga tca agc aag att tta aga Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser Ser Lys Ile Leu Arg 280 285 290	919
gct tct att tgg gaa act aat cct ggc aca ata aga att ttt tcc aac Ala Ser Ile Trp Glu Thr Asn Pro Gly Thr Ile Arg Ile Phe Ser Asn 295 300 305	967
caa gtt act gcc acc ttt ctt ata gaa tct gat gaa agt gat tat gtt Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp Glu Ser Asp Tyr Val 310 315 320 325	1015
ggc ttt aat gca aca tat act gca ttt aac agc agt gag ctt aat aat Gly Phe Asn Ala Thr Tyr Thr Ala Phe Asn Ser Ser Glu Leu Asn Asn 330 335 340	1063
tat gag aaa att aat tgt aac ttt gag gat ggc ttt tgt ttc tgg gtc Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly Phe Cys Phe Trp Val 345 350 355	1111
cag gat cta aat gat gat aat gaa tgg gaa agg att cag gga agc acc Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg Ile Gln Gly Ser Thr 360 365 370	1159
ttt tct cct ttt act gga ccc aat ttt gac cac act ttt ggc aat gct Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His Thr Phe Gly Asn Ala 375 380 385	1207
tca gga ttt tac att tct acc cca act gga cca gga ggg aga caa gaa Ser Gly Phe Tyr Ile Ser Thr Pro Thr Gly Pro Gly Gly Arg Gln Glu 390 395 400 405	1255

-62-

cga gtg ggg ctt tta agc ctc cct ttg gac ccc act ttg gag cca gct	1303
Arg Val Gly Leu Leu Ser Leu Pro Leu Asp Pro Thr Leu Glu Pro Ala	
410 415 420	
tgc ctt agt ttc tgg tat cat atg tat ggt gaa aat gtc cat aaa tta	1351
Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu Asn Val His Lys Leu	
425 430 435	
agc att aat atc agc aat gac caa aat atg gag aag aca gtt ttc caa	1399
Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu Lys Thr Val Phe Gln	
440 445 450	
aag gaa gga aat tat gga gac aat tgg aat tat gga caa gta acc cta	1447
Lys Glu Gly Asn Tyr Gly Asp Asn Trp Asn Tyr Gly Gln Val Thr Leu	
455 460 465	
aat gaa aca gtt aaa ttt aag gtt gct ttt aat gct ttt aaa aac aag	1495
Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn Ala Phe Lys Asn Lys	
470 475 480 485	
atc ctg agt gat att gcg ttg gat gac att agc cta aca tat ggg att	1543
Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser Leu Thr Tyr Gly Ile	
490 495 500	
tgc aat ggg agt ctt tat cca gaa cca act ttg gtg cca act cct cca	1591
Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu Val Pro Thr Pro Pro	
505 510 515	
cca gaa ctt cct acg gac tgt gga gga cct ttt gag ctg tgg gag cca	1639
Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe Glu Leu Trp Glu Pro	
520 525 530	
aat aca aca ttc agt tct acg aac ttt cca aac agc tac cct aat ctg	1687
Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn Ser Tyr Pro Asn Leu	
535 540 545	
gct ttc tgt gtt tgg att tta aat gca caa aaa gga aag aat ata caa	1735
Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys Gly Lys Asn Ile Gln	
550 555 560 565	
ctt cat ttt caa gaa ttt gac tta gaa aat att aac gat gta gtt gaa	1783
Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile Asn Asp Val Val Glu	
570 575 580	
ata aga gat ggt gaa gaa gct gat tcc ttg ctc tta gct gtg tac aca	1831
Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu Leu Ala Val Tyr Thr	
585 590 595	
ggg cct ggc cca gta aag gat gtg ttc tct acc acc aac aga atg act	1879
Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr Thr Asn Arg Met Thr	
600 605 610	
gtg ctt ctc atc act aac gat gtg ttg gca aga gga ggg ttt aaa gca	1927
Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg Gly Gly Phe Lys Ala	
615 620 625	
aac ttt act act ggc tat cac ttg ggg att cca gag cca tgc aag gca	1975
Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro Glu Pro Cys Lys Ala	
630 635 640 645	
gac cat ttt caa tgt aaa aat gga gag tgt gtt cca ctg gtg aat ctc	2023

-63-

Asp	His	Phe	Gln	Cys	Lys	Asn	Gly	Glu	Cys	Val	Pro	Leu	Val	Asn	Leu		
				650					655					660			
tgt	gac	ggt	cat	ctg	cac	tgt	gag	gat	ggc	tca	gat	gaa	gca	gat	tgt	2071	
Cys	Asp	Gly	His	Leu	His	Cys	Glu	Asp	Gly	Ser	Asp	Glu	Ala	Asp	Cys		
			665				670					675					
gtg	cgt	ttt	ttc	aat	ggc	aca	acg	aac	aac	aat	ggg	tta	gtg	cgg	ttc	2119	
Val	Arg	Phe	Phe	Asn	Gly	Thr	Thr	Asn	Asn	Asn	Gly	Leu	Val	Arg	Phe		
		680				685						690					
aga	atc	cag	agc	ata	tgg	cat	aca	gct	tgt	gct	gag	aac	tgg	acc	acc	2167	
Arg	Ile	Gln	Ser	Ile	Trp	His	Thr	Ala	Cys	Ala	Glu	Asn	Trp	Thr	Thr		
	695				700			705									
cag	att	tca	aat	gat	gtt	tgt	caa	ctg	ctg	gga	cta	ggg	agt	gga	aac	2215	
Gln	Ile	Ser	Asn	Asp	Val	Cys	Gln	Leu	Leu	Gly	Leu	Gly	Ser	Gly	Asn		
710					715			720							725		
tca	tca	aag	cca	atc	ttc	tct	acc	gat	ggg	gga	cca	ttt	gtc	aaa	tta	2263	
Ser	Ser	Lys	Pro	Ile	Phe	Ser	Thr	Asp	Gly	Gly	Pro	Phe	Val	Lys	Leu		
				730				735					740				
aac	aca	gca	cct	gat	ggc	cac	tta	ata	cta	aca	ccc	agt	caa	cag	tgt	2311	
Asn	Thr	Ala	Pro	Asp	Gly	His	Leu	Ile	Leu	Thr	Pro	Ser	Gln	Gln	Cys		
			745				750						755				
tta	cag	gat	tcc	ttg	att	cgg	tta	cag	tgt	aac	cat	aaa	tct	tgt	gga	2359	
Leu	Gln	Asp	Ser	Leu	Ile	Arg	Leu	Gln	Cys	Asn	His	Lys	Ser	Cys	Gly		
		760				765						770					
aaa	aaa	ctg	gca	gct	caa	gac	atc	acc	cca	aag	att	gtt	gga	gga	agt	2407	
Lys	Lys	Leu	Ala	Ala	Gln	Asp	Ile	Thr	Pro	Lys	Ile	Val	Gly	Gly	Ser		
	775				780						785						
aat	gcc	aaa	gaa	ggg	gcc	tgg	ccc	tgg	gtt	gtg	ggg	ctg	tat	tat	ggc	2455	
Asn	Ala	Lys	Glu	Gly	Ala	Trp	Pro	Trp	Val	Val	Gly	Leu	Tyr	Tyr	Gly		
790				795				800							805		
ggc	cga	ctg	ctc	tgc	ggc	gca	tct	ctc	gtc	agc	agt	gac	tgg	ctg	gtg	2503	
Gly	Arg	Leu	Leu	Cys	Gly	Ala	Ser	Leu	Val	Ser	Ser	Asp	Trp	Leu	Val		
				810				815					820				
tcc	gcc	gca	cac	tgc	gtg	tat	ggg	aga	aac	tta	gag	cca	tcc	aag	tgg	2551	
Ser	Ala	Ala	His	Cys	Val	Tyr	Gly	Arg	Asn	Leu	Glu	Pro	Ser	Lys	Trp		
			825				830						835				
aca	gca	atc	cta	ggc	ctg	cat	atg	aaa	tca	aat	ctg	acc	tct	cct	caa	2599	
Thr	Ala	Ile	Leu	Gly	Leu	His	Met	Lys	Ser	Asn	Leu	Thr	Ser	Pro	Gln		
		840				845						850					
aca	gtc	cct	cga	tta	ata	gat	gaa	att	gtc	ata	aac	cct	cat	tac	aat	2647	
Thr	Val	Pro	Arg	Leu	Ile	Asp	Glu	Ile	Val	Ile	Asn	Pro	His	Tyr	Asn		
	855				860						865						
agg	cga	aga	aag	gac	aac	gac	att	gcc	atg	atg	cat	ctg	gaa	ttt	aaa	2695	
Arg	Arg	Arg	Lys	Asp	Asn	Asp	Ile	Ala	Met	Met	His	Leu	Glu	Phe	Lys		
870				875				880							885		
gtg	aat	tac	aca	gat	tac	ata	caa	cct	att	tgt	tta	cgg	gaa	gaa	aat	2743	
Val	Asn	Tyr	Thr	Asp	Tyr	Ile	Gln	Pro	Ile	Cys	Leu	Pro	Glu	Glu	Asn		

-64-

890										895					900					
caa gtt ttt cct cca gga aga aat tgt tct att gct ggt tgg ggg acg	2791																			
Gln Val Phe Pro Pro Gly Arg Asn Cys Ser Ile Ala Gly Trp Gly Thr																				
905 910 915																				
gtt gta tat caa ggt act act gca aac ata ttg caa gaa gct gat gtt	2839																			
Val Val Tyr Gln Gly Thr Thr Ala Asn Ile Leu Gln Glu Ala Asp Val																				
920 925 930																				
cct ctt cta tca aat gag aga tgc caa cag cag atg cca gaa tat aac	2887																			
Pro Leu Leu Ser Asn Glu Arg Cys Gln Gln Gln Met Pro Glu Tyr Asn																				
935 940 945																				
att act gaa aat atg ata tgt gca ggc tat gaa gaa gga gga ata gat	2935																			
Ile Thr Glu Asn Met Ile Cys Ala Gly Tyr Glu Glu Gly Gly Ile Asp																				
950 955 960 965																				
tct tgt cag ggg gat tca gga gga cca tta atg tgc caa gaa aac aac	2983																			
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Cys Gln Glu Asn Asn																				
970 975 980																				
agg tgg ttc ctt gct ggt gtg acc tca ttt gga tac aag tgt gcc ctg	3031																			
Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly Tyr Lys Cys Ala Leu																				
985 990 995																				
cct aat cgc ccc gga gtg tat gcc agg gtc tca agg ttt acc gaa tgg	3079																			
Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser Arg Phe Thr Glu Trp																				
1000 1005 1010																				
ata caa agt ttt cta cat tag cgcatttctt aaactaaaca ggaaagtcgc	3130																			
Ile Gln Ser Phe Leu His *																				
1015																				
attattttcc cattotactc tagaaagcat ggaaattaag tgtttcgtac aaaaatttta	3190																			
aaaagttacc aaagggtttt attcttacot atgtcaatga aatgctaggg ggccagggaa	3250																			
acaaaatttt aaaaataata aaattcacca tagcaataca gaataacttt aaaataccat	3310																			
taaatacatt tgtattttcat tgtgaacagg tatttcttca cagatctcat ttttaaaatt	3370																			
cttaatgatt atttttatta cttactgttg tttaaaggga tgttatttta aagcatatac	3430																			
catacactta agaaatttga gcagaattta aaaaagaaag aaaataaatt gtttttccca	3490																			
aagtatgtca ctgttggaag taaactgcca taaattttct agttccagtt tagtttgctg	3550																			
ctattagcag aaactcaatt gtttctctgt tttttctatc aaaattttca acatatgcat	3610																			
aacottagta ttttcccaac caatagaaac tatttattgt aagcttatgt cacaggcctg	3670																			
gactaaattg attttacgtt cctctt	3696																			
<210> 31																				
<211> 1019																				
<212> PRT																				
<213> Homo Sapien																				
<400> 31																				
Met Gly Ser Lys Arg Gly Ile Ser Ser Arg His His Ser Leu Ser Ser																				
1 5 10 15																				
Tyr Glu Ile Met Phe Ala Ala Leu Phe Ala Ile Leu Val Val Leu Cys																				
20 25 30																				
Ala Gly Leu Ile Ala Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg																				
35 40 45																				
Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile																				
50 55 60																				
Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val																				
65 70 75 80																				

-65-

Asp	Phe	Lys	Val	Leu	Ala	Phe	Asp	Leu	Gln	Gln	Met	Ile	Asp	Glu	Ile
				85					90					95	
Phe	Leu	Ser	Ser	Asn	Leu	Lys	Asn	Glu	Tyr	Lys	Asn	Ser	Arg	Val	Leu
			100					105					110		
Gln	Phe	Glu	Asn	Gly	Ser	Ile	Ile	Val	Val	Phe	Asp	Leu	Phe	Phe	Ala
		115					120					125			
Gln	Trp	Val	Ser	Asp	Gln	Asn	Val	Lys	Glu	Glu	Leu	Ile	Gln	Gly	Leu
	130					135					140				
Glu	Ala	Asn	Lys	Ser	Ser	Gln	Leu	Val	Thr	Phe	His	Ile	Asp	Leu	Asn
145					150					155					160
Ser	Val	Asp	Ile	Leu	Asp	Lys	Leu	Thr	Thr	Thr	Ser	His	Leu	Ala	Thr
				165					170						175
Pro	Gly	Asn	Val	Ser	Ile	Glu	Cys	Leu	Pro	Gly	Ser	Ser	Pro	Cys	Thr
			180					185					190		
Asp	Ala	Leu	Thr	Cys	Ile	Lys	Ala	Asp	Leu	Phe	Cys	Asp	Gly	Glu	Val
		195					200					205			
Asn	Cys	Pro	Asp	Gly	Ser	Asp	Glu	Asp	Asn	Lys	Met	Cys	Ala	Thr	Val
	210					215					220				
Cys	Asp	Gly	Arg	Phe	Leu	Leu	Thr	Gly	Ser	Ser	Gly	Ser	Phe	Gln	Ala
225					230					235					240
Thr	His	Tyr	Pro	Lys	Pro	Ser	Glu	Thr	Ser	Val	Val	Cys	Gln	Trp	Ile
				245					250					255	
Ile	Arg	Val	Asn	Gln	Gly	Leu	Ser	Ile	Lys	Leu	Ser	Phe	Asp	Asp	Phe
			260					265					270		
Asn	Thr	Tyr	Tyr	Thr	Asp	Ile	Leu	Asp	Ile	Tyr	Glu	Gly	Val	Gly	Ser
		275				280						285			
Ser	Lys	Ile	Leu	Arg	Ala	Ser	Ile	Trp	Glu	Thr	Asn	Pro	Gly	Thr	Ile
	290					295					300				
Arg	Ile	Phe	Ser	Asn	Gln	Val	Thr	Ala	Thr	Phe	Leu	Ile	Glu	Ser	Asp
305					310					315					320
Glu	Ser	Asp	Tyr	Val	Gly	Phe	Asn	Ala	Thr	Tyr	Thr	Ala	Phe	Asn	Ser
				325					330					335	
Ser	Glu	Leu	Asn	Asn	Tyr	Glu	Lys	Ile	Asn	Cys	Asn	Phe	Glu	Asp	Gly
			340					345					350		
Phe	Cys	Phe	Trp	Val	Gln	Asp	Leu	Asn	Asp	Asp	Asn	Glu	Trp	Glu	Arg
		355					360						365		
Ile	Gln	Gly	Ser	Thr	Phe	Ser	Pro	Phe	Thr	Gly	Pro	Asn	Phe	Asp	His
	370					375					380				
Thr	Phe	Gly	Asn	Ala	Ser	Gly	Phe	Tyr	Ile	Ser	Thr	Pro	Thr	Gly	Pro
385					390					395					400
Gly	Gly	Arg	Gln	Glu	Arg	Val	Gly	Leu	Leu	Ser	Leu	Pro	Leu	Asp	Pro
				405					410					415	
Thr	Leu	Glu	Pro	Ala	Cys	Leu	Ser	Phe	Trp	Tyr	His	Met	Tyr	Gly	Glu
			420					425					430		
Asn	Val	His	Lys	Leu	Ser	Ile	Asn	Ile	Ser	Asn	Asp	Gln	Asn	Met	Glu
		435					440					445			
Lys	Thr	Val	Phe	Gln	Lys	Glu	Gly	Asn	Tyr	Gly	Asp	Asn	Trp	Asn	Tyr
	450					455					460				
Gly	Gln	Val	Thr	Leu	Asn	Glu	Thr	Val	Lys	Phe	Lys	Val	Ala	Phe	Asn
465					470					475					480
Ala	Phe	Lys	Asn	Lys	Ile	Leu	Ser	Asp	Ile	Ala	Leu	Asp	Asp	Ile	Ser
				485					490					495	
Leu	Thr	Tyr	Gly	Ile	Cys	Asn	Gly	Ser	Leu	Tyr	Pro	Glu	Pro	Thr	Leu
			500					505					510		
Val	Pro	Thr	Pro	Pro	Pro	Glu	Leu	Pro	Thr	Asp	Cys	Gly	Gly	Pro	Phe
		515					520						525		
Glu	Leu	Trp	Glu	Pro	Asn	Thr	Thr	Phe	Ser	Ser	Thr	Asn	Phe	Pro	Asn
	530					535					540				
Ser	Tyr	Pro	Asn	Leu	Ala	Phe	Cys	Val	Trp	Ile	Leu	Asn	Ala	Gln	Lys
545					550					555					560
Gly	Lys	Asn	Ile	Gln	Leu	His	Phe	Gln	Glu	Phe	Asp	Leu	Glu	Asn	Ile

-66-

Asn	Asp	Val	Val	565	Glu	Ile	Arg	Asp	Gly	570	Glu	Glu	Ala	Asp	Ser	575	Leu	Leu
Leu	Ala	Val	Tyr	580	Thr	Gly	Pro	Gly	585	Pro	Val	Lys	Asp	Val	Phe	590	Ser	Thr
Thr	Asn	Arg	Met	595	Thr	Val	Leu	Leu	600	Ile	Thr	Asn	Asp	Val	Leu	605	Ala	Arg
Gly	Gly	Phe	Lys	610	Ala	Asn	Phe	Thr	615	Thr	Gly	Tyr	His	Leu	Gly	620	Ile	Pro
625	Glu	Pro	Cys	630	Lys	Ala	Asp	His	635	Phe	Gln	Cys	Lys	Asn	Gly	640	Cys	Val
Pro	Leu	Val	Asn	645	Leu	Cys	Asp	Gly	650	His	Leu	His	Cys	Glu	Asp	655	Gly	Ser
Asp	Glu	Ala	Asp	660	Cys	Val	Arg	Phe	665	Phe	Asn	Gly	Thr	Thr	Asn	670	Asn	Asn
Gly	Leu	Val	Arg	675	Phe	Arg	Ile	Gln	680	Ser	Ile	Trp	His	Thr	Ala	685	Cys	Ala
Glu	Asn	Trp	Thr	690	Thr	Gln	Ile	Ser	695	Asn	Asp	Val	Cys	Gln	Leu	700	Leu	Gly
705	Leu	Gly	Ser	710	Gly	Asn	Ser	Ser	715	Lys	Pro	Ile	Phe	Ser	Thr	720	Asp	Gly
Pro	Phe	Val	Lys	725	Leu	Asn	Thr	Ala	730	Pro	Asp	Gly	His	Leu	Ile	735	Leu	Thr
Pro	Ser	Gln	Gln	740	Cys	Leu	Gln	Asp	745	Ser	Leu	Ile	Arg	Leu	Gln	750	Cys	Asn
His	Lys	Ser	Cys	755	Gly	Lys	Lys	Leu	760	Ala	Ala	Gln	Asp	Ile	Thr	765	Pro	Lys
Ile	Val	Gly	Gly	770	Ser	Asn	Ala	Lys	775	Glu	Gly	Ala	Trp	Pro	Trp	780	Val	Val
785	Gly	Leu	Tyr	790	Tyr	Gly	Gly	Arg	795	Leu	Leu	Cys	Gly	Ala	Ser	800	Val	Ser
Ser	Asp	Trp	Leu	805	Val	Ser	Ala	Ala	810	His	Cys	Val	Tyr	Gly	Arg	815	Asn	Leu
Glu	Pro	Ser	Lys	820	Trp	Thr	Ala	Ile	825	Leu	Gly	Leu	His	Met	Lys	830	Ser	Asn
Leu	Thr	Ser	Pro	835	Gln	Thr	Val	Pro	840	Arg	Leu	Ile	Asp	Glu	Ile	845	Val	Ile
Asn	Pro	His	Tyr	850	Asn	Arg	Arg	Lys	855	Asp	Asn	Asp	Ile	Ala	Met	860	Met	Met
865	His	Leu	Glu	870	Phe	Lys	Val	Asn	875	Tyr	Thr	Asp	Tyr	Ile	Gln	880	Ile	Cys
Leu	Pro	Glu	Glu	885	Asn	Gln	Val	Phe	890	Pro	Pro	Gly	Arg	Asn	Cys	895	Ser	Ile
Ala	Gly	Trp	Gly	900	Thr	Val	Val	Tyr	905	Gln	Gly	Thr	Thr	Ala	Asn	910	Ile	Leu
Gln	Glu	Ala	Asp	915	Val	Pro	Leu	Leu	920	Ser	Asn	Glu	Arg	Cys	Gln	925	Gln	Gln
Met	Pro	Glu	Tyr	930	Asn	Ile	Thr	Glu	935	Asn	Met	Ile	Cys	Ala	Gly	940	Tyr	Glu
945	Glu	Gly	Gly	950	Ile	Asp	Ser	Cys	955	Gln	Gly	Asp	Ser	Gly	Gly	960	Pro	Leu
Cys	Gln	Glu	Asn	965	Asn	Arg	Trp	Phe	970	Leu	Ala	Gly	Val	Thr	Ser	975	Phe	Gly
Tyr	Lys	Cys	Ala	980	Leu	Pro	Asn	Arg	985	Pro	Gly	Val	Tyr	Ala	Arg	990	Val	Ser
Arg	Phe	Thr	Glu	995	Trp	Ile	Gln	Ser	1000	Phe	Leu	His				1005		
1010									1015									

<210> 32
 <211> 1500
 <212> DNA

-67-

<213> Homo Sapien

<220>

<221> CDS

<222> (62)...(1318)

<223> Nucleotide sequence encoding human airway
trypsin-like protease

<300>

<308> GenBank AB002134

<309> 1998-06-04

<400> 32

gagtgggaat	ctcaaagcag	ttgagtaggc	agaaaaaaga	acctcttcat	taaggattaa	60
a atg tat agg cca gca cgt gta act tcg act tca aga ttt ctg aat cca	109					
Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro						
1 5 10 15						

tat gta gta tgt ttc att gtc gtc gca ggg gta gtg atc ctg gca gtc	157
Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val	
20 25 30	

acc ata gct cta ctt gtt tac ttt tta gct ttt gat caa aaa tct tac	205
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr	
35 40 45	

ttt tat agg agc agt ttt caa ctc cta aat gtt gaa tat aat agt cag	253
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln	
50 55 60	

tta aat tca cca gct aca cag gaa tac agg act ttg agt gga aga att	301
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile	
65 70 75 80	

gaa tct ctg att act aaa aca ttc aaa gaa tca aat tta aga aat cag	349
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln	
85 90 95	

ttc atc aga gct cat gtt gcc aaa ctg agg caa gat ggt agt ggt gtg	397
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val	
100 105 110	

aga gcg gat gtt gtc atg aaa ttt caa ttc act aga aat aac aat gga	445
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly	
115 120 125	

gca tca atg aaa agc aga att gag tct gtt tta cga caa atg ctg aat	493
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn	
130 135 140	

aac tct gga aac ctg gaa ata aac cct tca act gag ata aca tca ctt	541
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu	
145 150 155 160	

act gac cag gct gca gca aat tgg ctt att aat gaa tgt ggg gcc ggt	589
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly	
165 170 175	

cca gac cta ata aca ttg tct gag cag aga atc ctt gga ggc act gag	637
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu	
180 185 190	

-68-

gct gag gag gga agc tgg ccg tgg caa gtc agt ctg cgg ctc aat aat	685
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn	
195 200 205	
gcc cac cac tgt gga ggc agc ctg atc aat aac atg tgg atc ctg aca	733
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr	
210 215 220	
gca gct cac tgc ttc aga agc aac tct aat cct cgt gac tgg att gcc	781
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala	
225 230 235 240	
acg tct ggt att tcc aca aca ttt cct aaa cta aga atg aga gta aga	829
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg	
245 250 255	
aat att tta att cat aac aat tat aaa tct gca act cat gaa aat gac	877
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp	
260 265 270	
att gca ctt gtg aga ctt gag aac agt gtc acc ttt acc aaa gat atc	925
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile	
275 280 285	
cat agt gtg tgt ctc cca gct gct acc cag aat att cca cct ggc tct	973
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser	
290 295 300	
act gct tat gta aca gga tgg ggc gct caa gaa tat gct ggc cac aca	1021
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr	
305 310 315 320	
gtt cca gag cta agg caa gga cag gtc aga ata ata agt aat gat gta	1069
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val	
325 330 335	
tgt aat gca cca cat agt tat aat gga gcc atc ttg tct gga atg ctg	1117
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu	
340 345 350	
tgt gct gga gta cct caa ggt gga gtg gac gca tgt cag ggt gac tct	1165
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser	
355 360 365	
ggt ggc cca cta gta caa gaa gac tca cgg cgg ctt tgg ttt att gtg	1213
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val	
370 375 380	
ggg ata gta agc tgg gga gat cag tgt ggc ctg ccg gat aag cca gga	1261
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly	
385 390 395 400	
gtg tat act cga gtg aca gcc tac ctt gac tgg att agg caa caa act	1309
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr	
405 410 415	
ggg atc tag tgcaacaagt gcatccctgt tgcaaatgtct gtatgcaggt	1358
Gly Ile *	

-69-

```

gtgcctgtct taaattccaa agctttacat ttcaactgaa aaagaaacta gaaatgtcct 1418
aatttaacat cttgttacat aaatatggtt taacaaacac tgtttaacct ttctttatta 1478
ttaaagggtt tctattttct cc 1500

```

<210> 33
 <211> 418
 <212> PRT
 <213> Homo Sapien

<400> 33
 Met Tyr Arg Pro Ala Arg Val Thr Ser Thr Ser Arg Phe Leu Asn Pro
 1 5 10 15
 Tyr Val Val Cys Phe Ile Val Val Ala Gly Val Val Ile Leu Ala Val
 20 25 30
 Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
 35 40 45
 Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
 50 55 60
 Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
 65 70 75 80
 Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
 85 90 95
 Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
 100 105 110
 Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
 115 120 125
 Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
 130 135 140
 Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
 145 150 155 160
 Thr Asp Gln Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
 165 170 175
 Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
 180 185 190
 Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
 195 200 205
 Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
 210 215 220
 Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
 225 230 235 240
 Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
 245 250 255
 Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
 260 265 270
 Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
 275 280 285
 His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
 290 295 300
 Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
 305 310 315 320
 Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
 325 330 335
 Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
 340 345 350
 Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
 355 360 365
 Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
 370 375 380
 Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
 385 390 395 400
 Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr

-70-

Gly Ile 405 410 415
 <210> 34
 <211> 1783
 <212> DNA
 <213> Homo Sapien
 <220>
 <221> CDS
 <222> (246)...(1499)
 <223> Nucleic acid encoding human hepsin
 <300>
 <308> GenBank M18930
 <309> 1993-06-11
 <400> 34
 tcgagcccgc tttccaggga ccctacctga gggcccacag gtgaggcagc ctggcctagc 60
 aggccccacg ccaccgcctc tgccctccagg ccgcccgcctg ctgcgggggcc accatgctcc 120
 tgcccaggcc tggagactga cccgaccccg gcactacctc gaggtccgc cccacactgc 180
 tggaccccag ggtcccaccc tggcccagga ggtagccag ggaatcatta acaagaggca 240
 gtgac atg gcg cag aag gag ggt ggc cgg act gtg cca tgc tgc tcc aga 290
 Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg
 1 5 10 15
 ccc aag gtg gca gct ctc act gcg ggg acc ctg cta ctt ctg aca gcc 338
 Pro Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala
 20 25 30
 atc ggg gcg gca tcc tgg gcc att gtg gct gtt ctc ctc agg agt gac 386
 Ile Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp
 35 40 45
 cag gag ccg ctg tac cca gtg cag gtc agc tct gcg gac gct cgg ctc 434
 Gln Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu
 50 55 60
 atg gtc ttt gac aag acg gaa ggg acg tgg cgg ctg ctg tgc tcc tcg 482
 Met Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser
 65 70 75
 cgc tcc aac gcc agg gta gcc gga ctc agc tgc gag gag atg ggc ttc 530
 Arg Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe
 80 85 90 95
 ctc agg gca ctg acc cac tcc gag ctg gac gtg cga acg gcg ggc gcc 578
 Leu Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala
 100 105 110
 aat ggc acg tcg ggc ttc ttc tgt gtg gac gag ggg agg ctg ccc cac 626
 Asn Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His
 115 120 125
 acc cag agg ctg ctg gag gtc atc tcc gtg tgt gat tgc ccc aga ggc 674
 Thr Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly
 130 135 140
 cgt ttc ttg gcc gcc atc tgc caa gac tgt ggc cgc agg aag ctg ccc 722
 Arg Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro
 145 150 155

-71-

gtg gac cgc atc gtg gga ggc cgg gac acc agc ttg ggc cgg tgg ccg Val Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro 160 165 170 175	770
tgg caa gtc agc ctt cgc tat gat gga gca cac ctc tgt ggg gga tcc Trp Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser 180 185 190	818
ctg ctc tcc ggg gac tgg gtg ctg aca gcc gcc cac tgc ttc ccg gag Leu Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu 195 200 205	866
cgg aac cgg gtc ctg tcc cga tgg cga gtg ttt gcc ggt gcc gtg gcc Arg Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala 210 215 220	914
cag gcc tct ccc cac ggt ctg cag ctg ggg gtg cag gct gtg gtc tac Gln Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr 225 230 235	962
cac ggg ggc tat ctt ccc ttt cgg gac ccc aac agc gag gag aac agc His Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser 240 245 250 255	1010
aac gat att gcc ctg gtc cac ctc tcc agt ccc ctg ccc ctc aca gaa Asn Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu 260 265 270	1058
tac atc cag cct gtg tgc ctc cca gct gcc ggc cag gcc ctg gtg gat Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp 275 280 285	1106
ggc aag atc tgt acc gtg acg ggc tgg ggc aac acg cag tac tat ggc Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly 290 295 300	1154
caa cag gcc ggg gta ctc cag gag gct cga gtc ccc ata atc agc aat Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn 305 310 315	1202
gat gtc tgc aat ggc gct gac ttc tat gga aac cag atc aag ccc aag Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys 320 325 330 335	1250
atg ttc tgt gct ggc tac ccc gag ggt ggc att gat gcc tgc cag ggc Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly 340 345 350	1298
gac agc ggt ggt ccc ttt gtg tgt gag gac agc atc tct cgg acg cca Asp Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro 355 360 365	1346
cgt tgg cgg ctg tgt ggc att gtg agt tgg ggc act ggc tgt gcc ctg Arg Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu 370 375 380	1394
gcc cag aag cca ggc gtc tac acc aaa gtc agt gac ttc cgg gag tgg Ala Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp 385 390 395	1442

-72-

atc ttc cag gcc ata aag act cac tcc gaa gcc agc ggc atg gtg acc 1490
 ile phe gln ala ile lys thr his ser glu ala ser gly met val thr
 400 405 410 415

cag ctc tga ccggtggcctt ctcgctgcgc agcctccagg gcccgagggtg 1539
 gln leu *

atccccgtgg tgggatccac gctgggcccga ggatgggacg tttttcttct tgggcccggg 1599
 ccacaggtcc aaggacaccc tccctccagg gtcctctctt ccacagtggc gggcccactc 1659
 agccccgaga ccaccaacc tcaccctcct gacccccatg taaatattgt tctgctgtct 1719
 gggactcctg tctaggtgcc cctgatgatg ggatgctctt taaataataa agatggtttt 1779
 gatt 1783

<210> 35
 <211> 417
 <212> PRT
 <213> Homo Sapien

<400> 35
 Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro
 1 5 10 15
 Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile
 20 25 30
 Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
 35 40 45
 Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
 50 55 60
 Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
 65 70 75 80
 Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
 85 90 95
 Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
 100 105 110
 Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
 115 120 125
 Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
 130 135 140
 Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
 145 150 155 160
 Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
 165 170 175
 Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
 180 185 190
 Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
 195 200 205
 Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
 210 215 220
 Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
 225 230 235 240
 Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
 245 250 255
 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
 260 265 270
 Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
 275 280 285
 Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
 290 295 300
 Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
 305 310 315 320
 Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met

-73-

```

          325          330          335
Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
          340          345          350
Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
          355          360          365
Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
          370          375          380
Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
          385          390          395          400
Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
          405          410          415
Leu

```

<210> 36
 <211> 2479
 <212> DNA
 <213> Homo sapien

<220>
 <221> CDS
 <222> (57)...(1535)
 <223> Nucleotide sequence encoding human serine protease (TMPRS2)

<300>
 <308> GenBank U75329
 <309> 1997-10-10

```

<400> 36
gtcatattga acattccaga tacctatcat tactcgatgc tgttgataac agcaag atg      59
                                         Met
                                         1

gct ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac      107
Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn
          5          10          15

cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc      155
His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val
          20          25          30

ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg      203
Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val
          35          40          45

ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc      251
Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val
          50          55          60          65

tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act      299
Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr
          70          75          80

aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga      347
Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly
          85          90          95

gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc      395
Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys
          100          105          110

tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc      443

```

-74-

Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn	Pro		
115						120					125						
tct	aac	tgg	tgt	gat	ggc	gtg	tca	cac	tgc	ccc	ggc	ggg	gag	gac	gag	491	
Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp	Glu		
130					135					140					145		
aat	cgg	tgt	gtt	cgc	ctc	tac	gga	cca	aac	ttc	atc	ctt	cag	atg	tac	539	
Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met	Tyr		
				150					155					160			
tca	tct	cag	agg	aag	tcc	tgg	cac	cct	gtg	tgc	caa	gac	gac	tgg	aac	587	
Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp	Asn		
			165					170					175				
gag	aac	tac	ggg	cgg	gcg	gcc	tgc	agg	gac	atg	ggc	tat	aag	aat	aat	635	
Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn	Asn		
		180					185					190					
ttt	tac	tct	agc	caa	gga	ata	gtg	gat	gac	agc	gga	tcc	acc	agc	ttt	683	
Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser	Phe		
	195					200					205						
atg	aaa	ctg	aac	aca	agt	gcc	ggc	aat	gtc	gat	atc	tat	aaa	aaa	ctg	731	
Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys	Leu		
210					215					220					225		
tac	cac	agt	gat	gcc	tgt	tct	tca	aaa	gca	gtg	gtt	tct	tta	cgc	tgt	779	
Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg	Cys		
				230					235					240			
tta	gcc	tgc	ggg	gtc	aac	ttg	aac	tca	agc	cgc	cag	agc	agg	atc	gtg	827	
Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile	Val		
			245					250					255				
ggc	ggt	gag	agc	gcg	ctc	ccg	ggg	gcc	tgg	ccc	tgg	cag	gtc	agc	ctg	875	
Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser	Leu		
		260					265				270						
cac	gtc	cag	aac	gtc	cac	gtg	tgc	gga	ggc	tcc	atc	atc	acc	ccc	gag	923	
His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro	Glu		
	275					280					285						
tgg	atc	gtg	aca	gcc	gcc	cac	tgc	gtg	gaa	aaa	cct	ctt	aac	aat	cca	971	
Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn	Pro		
290					295					300					305		
tgg	cat	tgg	acg	gca	ttt	gcg	ggg	att	ttg	aga	caa	tct	ttc	atg	ttc	1019	
Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met	Phe		
				310					315					320			
tat	gga	gcc	gga	tac	caa	gta	caa	aaa	gtg	att	tct	cat	cca	aat	tat	1067	
Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn	Tyr		
			325					330					335				
gac	tcc	aag	acc	aag	aac	aat	gac	att	gcg	ctg	atg	aag	ctg	cag	aag	1115	
Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Lys		
		340					345					350					
cct	ctg	act	ttc	aac	gac	cta	gtg	aaa	cca	gtg	tgt	ctg	ccc	aac	cca	1163	
Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn	Pro		

-75-

355	360	365	
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg			1211
Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly			
370	375	380	385
gcc acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag			1259
Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys			
	390	395	400
gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac			1307
Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp			
	405	410	415
aac ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac			1355
Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn			
	420	425	430
gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tog aac			1403
Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Asn			
	435	440	445
aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt			1451
Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys			
	450	455	460
gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg			1499
Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr			
	470	475	480
gac tgg att tat cga caa atg aag gca aac ggc taa tccacatggt			1545
Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly *			
	485	490	
cttcgtcctt gacgtcgttt tacaagaaaa caatggggct ggttttgctt ccccggtgcat			1605
gatttactct tagagatgat tcagaggtca cttcattttt attaaacagt gaacttgtct			1665
ggctttggca ctctctgcca tactgtgcag gctgcagtgg ctcccctgcc cagcctgctc			1725
tccctaacc cttgtccgca aggggtgatg gccggctggt tgtggggcact ggcgggtcaat			1785
tgtggaagga agaggggttg aggctgcccc cattgagatc ttccctgctga gtcctttcca			1845
ggggccaatt ttggatgagc atggagctgt cacttctcag ctgctggatg acttgagatg			1905
aaaaaggaga gacatggaaa gggagacagc cagggtggcac ctgcagcggc tgccctctgg			1965
ggccacttgg tagtgtcccc agcctacttc acaaggggat ttgtctgatg gggttcttaga			2025
gccttagcag ccctggatgg tggccagaaa taaagggacc agcccttcat gggtgggtgac			2085
gtggttagtca cttgtaaggg gaacagaaac atttttgttc ttatgggggtg agaatataga			2145
cagtgcctt ggtgcgaggg aagcaattga aaaggaactt gccctgagca ctccctggtgc			2205
aggtctccac ctgcacattg ggtggggctc ctgggagggg gactcagcct tccctcctcat			2265
cctcccctgac cctgctccta gcaccctgga gagtgaatgc cccttggtcc ctggcagggc			2325
gccaagtttg gcaccatgtc ggcctcttca ggccctgatag tcattggaaa ttgaggtcca			2385
tgggggaaat caaggatgct cagtttaagg tacactgttt ccatgttatg tttctacaca			2445
ttgatgggtg tgaccctgag ttcaaagcca tctt			2479

<210> 37

<211> 492

<212> PRT

<213> Homo sapien

<400> 37

Met	Ala	Leu	Asn	Ser	Gly	Ser	Pro	Pro	Ala	Ile	Gly	Pro	Tyr	Tyr	Glu
1			5				10					15			
Asn	His	Gly	Tyr	Gln	Pro	Glu	Asn	Pro	Tyr	Pro	Ala	Gln	Pro	Thr	Val
	20						25					30			

-76-

Val	Pro	Thr	Val	Tyr	Glu	Val	His	Pro	Ala	Gln	Tyr	Tyr	Pro	Ser	Pro
		35					40					45			
Val	Pro	Gln	Tyr	Ala	Pro	Arg	Val	Leu	Thr	Gln	Ala	Ser	Asn	Pro	Val
	50					55					60				
Val	Cys	Thr	Gln	Pro	Lys	Ser	Pro	Ser	Gly	Thr	Val	Cys	Thr	Ser	Lys
65					70					75					80
Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val
				85					90					95	
Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys
			100					105					110		
Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
		115					120					125			
Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
		130				135					140				
Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
145					150					155					160
Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
				165					170					175	
Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn
			180					185					190		
Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
		195					200					205			
Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys
		210				215					220				
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg
225					230					235					240
Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
				245					250					255	
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
			260					265					270		
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro
		275					280					285			
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met
305					310					315					320
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn
				325					330					335	
Tyr	Asp	Ser	Lys	Thr	Lys	Asn	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln
			340					345					350		
Lys	Pro	Leu	Thr	Phe	Asn	Asp	Leu	Val	Lys	Pro	Val	Cys	Leu	Pro	Asn
		355					360					365			
Pro	Gly	Met	Met	Leu	Gln	Pro	Glu	Gln	Leu	Cys	Trp	Ile	Ser	Gly	Trp
	370					375					380				
Gly	Ala	Thr	Glu	Glu	Lys	Gly	Lys	Thr	Ser	Glu	Val	Leu	Asn	Ala	Ala
385					390					395					400
Lys	Val	Leu	Leu	Ile	Glu	Thr	Gln	Arg	Cys	Asn	Ser	Arg	Tyr	Val	Tyr
				405					410					415	
Asp	Asn	Leu	Ile	Thr	Pro	Ala	Met	Ile	Cys	Ala	Gly	Phe	Leu	Gln	Gly
		420						425					430		
Asn	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Thr	Ser
		435					440					445			
Asn	Asn	Asn	Ile	Trp	Trp	Leu	Ile	Gly	Asp	Thr	Ser	Trp	Gly	Ser	Gly
	450					455					460				
Cys	Ala	Lys	Ala	Tyr	Arg	Pro	Gly	Val	Tyr	Gly	Asn	Val	Met	Val	Phe
465					470					475					480
Thr	Asp	Trp	Ile	Tyr	Arg	Gln	Met	Lys	Ala	Asn	Gly				
				485					490						

<210> 38

<211> 2079

-77-

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (251)...(1522)

<223> Nucleotide sequence encoding transmembrane
protease, serine 4 (TMPRSS4)

<300>

<308> GenBank NM016425

<309> 2000-11-06

<400> 38

gagagggcagc agcttggttca gcggaacaagg atgctgggagc tgagggacca aggcctgccc	60
tgcactcggg cctcctccag ccagtgtga ccagggactt ctgacctgct ggccagccag	120
gacctgtgtg gggaggccct cctgtgtgct tgggggtgaca atctcagctc caggctacag	180
ggagaccggg aggatcacag agccagcatg gtacaggatc ctgacagtga tcaacctctg	240
aacagcctcg atg tca aac ccc tgc gca aac ccc gta tcc cca tgg aga	289
Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg	
1 5 10	
cct tca gaa agt gtg ggg atc ccc atc atc ata gca cta ctg agc ctg	337
Pro Ser Glu Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu	
15 20 25	
gcg agt atc atc att gtg gtt gtc ctc atc aag gtg att ctg gat aaa	385
Ala Ser Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys	
30 35 40 45	
tac tac ttc ctc tgc ggg cag cct ctc cac ttc atc ccg agg aag cag	433
Tyr Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln	
50 55 60	
ctg tgt gac gga gag ctg gac tgt ccc ttg ggg gag gac gag gag cac	481
Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His	
65 70 75	
tgt gtc aag agc ttc ccc gaa ggg cct gca gtg gca gtc cgc ctc tcc	529
Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser	
80 85 90	
aag gac cga tcc aca ctg cag gtg ctg gac tgc gcc aca ggg aac tgg	577
Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp	
95 100 105	
ttc tct gcc tgt ttc gac aac ttc aca gaa gct ctc gct gag aca gcc	625
Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala	
110 115 120 125	
tgt agg cag atg ggc tac agc agc aaa ccc act ttc aga gct gtg gag	673
Cys Arg Gln Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu	
130 135 140	
att ggc cca gac cag gat ctg gat gtt gtt gaa atc aca gaa aac agc	721
Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser	
145 150 155	
cag gag ctt cgc atg cgg aac tca agt ggg ccc tgt ctc tca ggc tcc	769
Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser	
160 165 170	

-78-

ctg gtc tcc ctg cac tgt ctt gcc tgt ggg aag agc ctg aag acc ccc Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro 175 180 185	817
cgt gtg gtg ggt ggg gag gag gcc tct gtg gat tct tgg cct tgg cag Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln 190 195 200 205	865
gtc agc atc cag tac gac aaa cag cac gtc tgt gga ggg agc atc ctg Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu 210 215 220	913
gac ccc cac tgg gtc ctc acg gca gcc cac tgc ttc agg aaa cat acc Asp Pro His Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr 225 230 235	961
gat gtg ttc aac tgg aag gtg cgg gca ggc tca gac aaa ctg ggc agc Asp Val Phe Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser 240 245 250	1009
ttc cca tcc ctg gct gtg gcc aag atc atc atc att gaa ttc aac ccc Phe Pro Ser Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro 255 260 265	1057
atg tac ccc aaa gac aat gac atc gcc ctc atg aag ctg cag ttc cca Met Tyr Pro Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro 270 275 280 285	1105
ctc act ttc tca ggc aca gtc agg ccc atc tgt ctg ccc ttc ttt gat Leu Thr Phe Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp 290 295 300	1153
gag gag ctc act cca gcc acc cca ctc tgg atc att gga tgg ggc ttt Glu Glu Leu Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe 305 310 315	1201
acg aag cag aat gga ggg aag atg tct gac ata ctg ctg cag gcg tca Thr Lys Gln Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser 320 325 330	1249
gtc cag gtc att gac agc aca cgg tgc aat gca gac gat gcg tac cag Val Gln Val Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln 335 340 345	1297
ggg gaa gtc acc gag aag atg atg tgt gca ggc atc ccg gaa ggg ggt Gly Glu Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly 350 355 360 365	1345
gtg gac acc tgc cag ggt gac agt ggt ggg ccc ctg atg tac caa tct Val Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser 370 375 380	1393
gac cag tgg cat gtg gtg ggc atc gtt agc tgg ggc tat ggc tgc ggg Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly 385 390 395	1441
ggc ccg agc acc cca gga gta tac acc aag gtc tca gcc tat ctc aac Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn 400 405 410	1489

-79-

tgg atc tac aat gtc tgg aag gct gag ctg taa tgctgctgcc cctttgcagt 1542
 Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu *
 415 420

gctgggagcc gcttccttcc tgccttgccc acctggggat cccccaaagt cagacacaga 1602
 gcaagagtc ccttgggtac acccctctgc ccacagcctc agcatttctt ggagcagcaa 1662
 agggcctcaa ttcctgtaag agaccctcgc agcccagagg cgcccagagg aagtcagcag 1722
 ccctagctcg gccacacttg gtgctcccag catcccaggg agagacacag cccactgaac 1782
 aaggctcag ggggtattgct aagccaagaa ggaactttcc cacactactg aatggaagca 1842
 ggctgtcttg taaaagccca gatcactgtg ggctggagag gagaaggaaa gggctctgcgc 1902
 cagccctgtc cgtcttcacc catccccaag cctactagag caagaaacca gttgtaatat 1962
 aaaatgcact gccctactgt tggatgact accgttacct actgttgtca ttgttattac 2022
 agctatggcc actattatta aagagctgtg taacatcaaa aaaaaaaaaa aaaaaaa 2079

<210> 39
 <211> 423
 <212> PRT
 <213> Homo sapien

<400> 39
 Met Ser Asn Pro Cys Ala Asn Pro Val Ser Pro Trp Arg Pro Ser Glu
 1 5 10 15
 Ser Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile
 20 25 30
 Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe
 35 40 45
 Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp
 50 55 60
 Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys
 65 70 75 80
 Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg
 85 90 95
 Ser Thr Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala
 100 105 110
 Cys Phe Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln
 115 120 125
 Met Gly Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro
 130 135 140
 Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu
 145 150 155 160
 Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser
 165 170 175
 Leu His Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val
 180 185 190
 Gly Gly Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile
 195 200 205
 Gln Tyr Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His
 210 215 220
 Trp Val Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe
 225 230 235 240
 Asn Trp Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser
 245 250 255
 Leu Ala Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro
 260 265 270
 Lys Asp Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe
 275 280 285
 Ser Gly Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu
 290 295 300
 Thr Pro Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln
 305 310 315 320
 Asn Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val

-80-

Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	Val
			340					345					350		
Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	Asp	Thr
		355					360					365			
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	Asp	Gln	Trp
		370				375					380				
His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	Gly	Gly	Pro	Ser
385					390					395					400
Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	Leu	Asn	Trp	Ile	Tyr
			405						410					415	
Asn	Val	Trp	Lys	Ala	Glu	Leu									
			420												

<210> 40
 <211> 1471
 <212> DNA
 <213> Artificial sequence

<220>
 <223> DESC1 gene

<221> misc feature
 <222> (626)...(1324)
 <223> protease domain

<221> CDS
 <222> (56)...(1324)

<400> 40	
tgacttggat gtagacctcg accttcacag gactcttcat tgctgggttg caatg atg	58
	Met
	1
tat cgg cca gat gtg gtg agg gct agg aaa aga gtt tgt tgg gaa ccc	106
Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu Pro	
	5 10 15
tgg gtt atc ggc ctc gtc ats ttc ata tcc ctg att gtc ctg gca gtg	154
Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala Val	
	20 25 30
tgc att gga stc act gtt cat tat gtg aga tat aat caa aag aag acc	202
Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys Thr	
	35 40 45
tac aat tac tat agc aca ttg tca ttt aca act gac aaa cta tat gct	250
Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr Ala	
	50 55 60 65
gag ttt ggc aga gag gct tct aac aat ttt aca gaa atg agc cag aga	298
Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln Arg	
	70 75 80
ctt gaa tca atg gtg aaa aat gca ttt tat aaa tct cca tta agg gaa	346
Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg Glu	
	85 90 95
gaa ttt gtc aag tct cag gtt atc aag ttc agt caa cag aag cat gga	394
Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His Gly	
	100 105 110

-81-

gtg	ttg	gct	cat	atg	ctg	ttg	att	tgt	aga	ttt	cac	tct	act	gag	gat	442
Val	Leu	Ala	His	Met	Leu	Leu	Ile	Cys	Arg	Phe	His	Ser	Thr	Glu	Asp	
	115					120					125					
cct	gaa	act	gta	gat	aaa	att	gtt	caa	ctt	gtt	tta	cat	gaa	aag	ctg	490
Pro	Glu	Thr	Val	Asp	Lys	Ile	Val	Gln	Leu	Val	Leu	His	Glu	Lys	Leu	
130					135					140					145	
caa	gat	gct	gta	gga	ccc	cct	aaa	gta	gat	cct	cac	tca	gtt	aaa	att	538
Gln	Asp	Ala	Val	Gly	Pro	Pro	Lys	Val	Asp	Pro	His	Ser	Val	Lys	Ile	
				150					155					160		
aaa	aaa	atc	aac	aag	aca	gaa	aca	gac	agc	tat	cta	aac	cat	tgc	tgc	586
Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys	Cys	
			165					170					175			
gga	aca	cga	aga	agt	aaa	act	cta	ggg	cag	agt	ctc	agg	atc	gtt	ggg	634
Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val	Gly	
		180					185					190				
ggg	aca	gaa	gta	gaa	gag	ggg	gaa	tgg	ccc	tgg	cag	gct	agc	ctg	cag	682
Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	
		195				200					205					
tgg	gat	ggg	agt	cat	cgc	tgt	gga	gca	acc	tta	att	aat	gcc	aca	tgg	730
Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr	Trp	
210					215					220					225	
ctt	gtg	agt	gct	gct	cac	tgt	ttt	aca	aca	tat	aag	aac	cct	gcc	aga	778
Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala	Arg	
				230					235					240		
tgg	act	gct	tcc	ttt	gga	gta	aca	ata	aaa	cct	tcg	aaa	atg	aaa	cgg	826
Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys	Arg	
			245					250					255			
ggg	ctc	cgg	aga	ata	att	gtc	cat	gaa	aaa	tac	aaa	cac	cca	tca	cat	874
Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser	His	
		260					265					270				
gac	tat	gat	att	tct	ctt	gca	gag	ctt	tct	agc	cct	gtt	ccc	tac	aca	922
Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr	Thr	
	275					280					285					
aat	gca	gta	cat	aga	gtt	tgt	ctc	cct	gat	gca	tcc	tat	gag	ttt	caa	970
Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe	Gln	
290					295					300					305	
cca	ggg	gat	gtg	atg	ttt	gtg	aca	gga	ttt	gga	gca	ctg	aaa	aat	gat	1018
Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	Phe	Gly	Ala	Leu	Lys	Asn	Asp	
				310					315					320		
ggg	tac	agt	caa	aat	cat	ctt	cga	caa	gca	cag	gtg	act	ctc	ata	gac	1066
Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	
			325					330					335			
gct	aca	act	tgc	aat	gaa	cct	caa	gct	tac	aat	gac	gcc	ata	act	cct	1114
Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	
		340					345					350				

-82-

```

aga atg tta tgt gct ggc tcc tta gaa gga aaa aca gat gca tgc cag      1162
Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln
    355                      360                      365

ggt gac tct gga gga cca ctg gtt agt tca gat gct aga gat atc tgg      1210
Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp
    370                      375                      380                      385

tac ctt gct gga ata gtg agc tsg gga gat gaa tgt gcg aaa ccc aac      1258
Tyr Leu Ala Gly Ile Val Ser Xaa Gly Asp Glu Cys Ala Lys Pro Asn
                      390                      395                      400

aag cct ggt gtt tat act aga gtt acg gcc ttg cgg gac tgg att act      1306
Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr
                      405                      410                      415

tca aaa act ggt atc taa gagagaaaag cctcatggaa cagataacat      1354
Ser Lys Thr Gly Ile *
    420

ttttttttgt tttttgggtg tggaggccat ttttagagat acagaattgg agaagacttg      1414
caaaacagct agatttgact gatctcaata aactgtttgc ttgatgcaaa aaaaaaa      1471

<210> 41
<211> 422
<212> PRT
<213> Homo Sapien

<220>
<221> VARIANT
<222> 24
<223> Xaa is Ile or Met

<221> VARIANT
<222> 37
<223> Xaa is Leu or Val

<221> VARIANT
<222> 393
<223> Xaa is Ser or Trp

<400> 41
Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
 1                      5                      10                      15
Pro Trp Val Ile Gly Leu Val Xaa Phe Ile Ser Leu Ile Val Leu Ala
    20                      25                      30
Val Cys Ile Gly Xaa Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
    35                      40                      45
Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
    50                      55                      60
Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
    65                      70                      75                      80
Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
    85                      90                      95
Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
    100                      105                      110
Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
    115                      120                      125
Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
    130                      135                      140
Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys

```

-83-

145		150		155		160									
Ile	Lys	Lys	Ile	Asn	Lys	Thr	Glu	Thr	Asp	Ser	Tyr	Leu	Asn	His	Cys
				165					170					175	
Cys	Gly	Thr	Arg	Arg	Ser	Lys	Thr	Leu	Gly	Gln	Ser	Leu	Arg	Ile	Val
			180						185				190		
Gly	Gly	Thr	Glu	Val	Glu	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu
		195					200					205			
Gln	Trp	Asp	Gly	Ser	His	Arg	Cys	Gly	Ala	Thr	Leu	Ile	Asn	Ala	Thr
	210				215						220				
Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	Ala
225				230					235						240
Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	Met	Lys
			245						250					255	
Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	His	Pro	Ser
		260						265					270		
His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	Pro	Val	Pro	Tyr
	275					280						285			
Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	Ala	Ser	Tyr	Glu	Phe
	290					295					300				
Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	Phe	Gly	Ala	Leu	Lys	Asn
305				310					315						320
Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	Gln	Ala	Gln	Val	Thr	Leu	Ile
			325						330					335	
Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr
		340						345					350		
Pro	Arg	Met	Leu	Cys	Ala	Gly	Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys
	355					360						365			
Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile
	370					375					380				
Trp	Tyr	Leu	Ala	Gly	Ile	Val	Ser	Xaa	Gly	Asp	Glu	Cys	Ala	Lys	Pro
385				390					395						400
Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile
			405						410					415	
Thr	Ser	Lys	Thr	Gly	Ile										
			420												

<210> 42

<211> 1257

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(1257)

<223> Nucleotide sequence encoding MTSP9

<400> 42

atg	atg	tat	cgg	aca	gta	gga	ttt	ggc	acc	cga	agc	aga	aat	ctg	aag	48
Met	Met	Tyr	Arg	Thr	Val	Gly	Phe	Gly	Thr	Arg	Ser	Arg	Asn	Leu	Lys	
1				5				10						15		

cca	tgg	atg	att	gcc	gtt	ctc	att	gtg	ttg	tcc	ctg	aca	gtg	gtg	gca	96
Pro	Trp	Met	Ile	Ala	Val	Leu	Ile	Val	Leu	Ser	Leu	Thr	Val	Val	Ala	
			20					25					30			

gtg	acc	ata	ggt	ctc	ctg	gtt	cac	ttc	cta	gta	ttt	gac	caa	aaa	aag	144
Val	Thr	Ile	Gly	Leu	Leu	Val	His	Phe	Leu	Val	Phe	Asp	Gln	Lys	Lys	
			35				40					45				

gag	tac	tat	cat	ggc	tcc	ttt	aaa	att	tta	gat	cca	caa	atc	aat	aac	192
Glu	Tyr	Tyr	His	Gly	Ser	Phe	Lys	Ile	Leu	Asp	Pro	Gln	Ile	Asn	Asn	

-84-

50	55	60	
aat ttc gga caa agc aac aca tat caa ctt aag gac tta cga gag acg Asn Phe Gly Gln Ser Asn Thr Tyr Gln Leu Lys Asp Leu Arg Glu Thr 65 70 75 80			240
acc gaa aat ttg gtg gat gag ata ttt ata gat tca gcc tgg aag aaa Thr Glu Asn Leu Val Asp Glu Ile Phe Ile Asp Ser Ala Trp Lys Lys 85 90 95			288
aat tat atc aag aac caa gta gtc aga ctg act cca gag gaa gat ggt Asn Tyr Ile Lys Asn Gln Val Val Arg Leu Thr Pro Glu Glu Asp Gly 100 105 110			336
gtg aaa gta gat gtc att atg gtg ttc cag ttc ccc tct act gaa caa Val Lys Val Asp Val Ile Met Val Phe Gln Phe Pro Ser Thr Glu Gln 115 120 125			384
agg gca gta aga gag aag aaa atc caa agc atc tta aat cag aag ata Arg Ala Val Arg Glu Lys Lys Ile Gln Ser Ile Leu Asn Gln Lys Ile 130 135 140			432
agg aat tta aga gcc ttg cca ata aat gcc tca tca gtt caa gtt aat Arg Asn Leu Arg Ala Leu Pro Ile Asn Ala Ser Ser Val Gln Val Asn 145 150 155 160			480
gca atg agc tca tca aca ggg gag tta act gtc caa gca agt tgt ggt Ala Met Ser Ser Thr Gly Glu Leu Thr Val Gln Ala Ser Cys Gly 165 170 175			528
aaa cga gtt gtt cca tta aac gtc aac aga ata gca tct gga gtc att Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile 180 185 190			576
gca ccc aag gcg gcc tgg cct tgg caa gct tcc ctt cag tat gat aac Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn 195 200 205			624
atc cat cag tgt ggg gcc acc ttg att agt aac aca tgg ctt gtc act Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr 210 215 220			672
gca gca cac tgc ttc cag aag tat aaa aat cca cat caa tgg act gtt Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val 225 230 235 240			720
agt ttt gga aca aaa atc aac cct ccc tta atg aaa aga aat gtc aga Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg 245 250 255			768
aga ttt att atc cat gag aag tac cgc tct gca gca aga gag tac gac Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp 260 265 270			816
att gct gtt gtg cag gtc tct tcc aga gtc acc ttt tgg gat gac ata Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile 275 280 285			864
cgc cgg att tgt ttg cca gaa gcc tct gca tcc ttc caa cca aat ttg Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu 290 295 300			912

-85-

act gtc cac atc aca gga ttt gga gca ctt tac tat ggt ggg gaa tcc	960
Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser	
305 310 315 320	
caa aat gat ctc cga gaa gcc aga gtg aaa atc ata agt gac gat gtc	1008
Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val	
325 330 335	
tgc aag caa cca cag gtg tat ggc aat gat ata aaa cct gga atg ttc	1056
Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe	
340 345 350	
tgt gcc gga tat atg gaa gga att tat gat gcc tgc agg ggt gat tct	1104
Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser	
355 360 365	
ggg gga cct tta gtc aca agg gat ctg aaa gat acg tgg tat ctc att	1152
Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile	
370 375 380	
gga att gta agc tgg gga gat aac tgt ggt caa aag gac aag cct gga	1200
Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly	
385 390 395 400	
gtc tac aca caa gtg act tat tac cga aac tgg att gct tca aaa aca	1248
Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr	
405 410 415	
ggc atc taa	1257
Gly Ile *	

<210> 43
 <211> 418
 <212> PRT
 <213> Homo sapien

<400> 43	
Met Met Tyr Arg Thr Val Gly Phe Gly Thr Arg Ser Arg Asn Leu Lys	
1 5 10 15	
Pro Trp Met Ile Ala Val Leu Ile Val Leu Ser Leu Thr Val Val Ala	
20 25 30	
Val Thr Ile Gly Leu Leu Val His Phe Leu Val Phe Asp Gln Lys Lys	
35 40 45	
Glu Tyr Tyr His Gly Ser Phe Lys Ile Leu Asp Pro Gln Ile Asn Asn	
50 55 60	
Asn Phe Gly Gln Ser Asn Thr Tyr Gln Leu Lys Asp Leu Arg Glu Thr	
65 70 75 80	
Thr Glu Asn Leu Val Asp Glu Ile Phe Ile Asp Ser Ala Trp Lys Lys	
85 90 95	
Asn Tyr Ile Lys Asn Gln Val Val Arg Leu Thr Pro Glu Glu Asp Gly	
100 105 110	
Val Lys Val Asp Val Ile Met Val Phe Gln Phe Pro Ser Thr Glu Gln	
115 120 125	
Arg Ala Val Arg Glu Lys Lys Ile Gln Ser Ile Leu Asn Gln Lys Ile	
130 135 140	
Arg Asn Leu Arg Ala Leu Pro Ile Asn Ala Ser Ser Val Gln Val Asn	
145 150 155 160	
Ala Met Ser Ser Ser Thr Gly Glu Leu Thr Val Gln Ala Ser Cys Gly	
165 170 175	

-86-

Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val Ile
 180 185 190
 Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp Asn
 195 200 205
 Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val Thr
 210 215 220
 Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr Val
 225 230 235 240
 Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val Arg
 245 250 255
 Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr Asp
 260 265 270
 Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp Ile
 275 280 285
 Arg Arg Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn Leu
 290 295 300
 Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu Ser
 305 310 315 320
 Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp Val
 325 330 335
 Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met Phe
 340 345 350
 Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp Ser
 355 360 365
 Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu Ile
 370 375 380
 Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro Gly
 385 390 395 400
 Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys Thr
 405 410 415
 Gly Ile

<210> 44

<211> 2130

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (0)...(2104)

<223> Nucleotide sequence encoding MTSP10, including
MTSP10 protease domain

<400> 44

ata aac ctg gtt tat aca aca tct gcc ttc tcc aaa ttt tat gag cag	48
Ile Asn Leu Val Tyr Thr Thr Ser Ala Phe Ser Lys Phe Tyr Glu Gln	
1 5 10 15	
tct gtt gtt gca gat gtc agc agc aac aac aaa ggc ggc ctc ctt gtc	96
Ser Val Val Ala Asp Val Ser Ser Asn Asn Lys Gly Gly Leu Leu Val	
20 25 30	
cac ttt tgg att gtt ttt gtc atg cca cgt gcc aaa ggc cac atc ttc	144
His Phe Trp Ile Val Phe Val Met Pro Arg Ala Lys Gly His Ile Phe	
35 40 45	
tgt gaa gac tgt gtt gcc gcc atc ttg aag gac tcc atc cag aca agc	192
Cys Glu Asp Cys Val Ala Ala Ile Leu Lys Asp Ser Ile Gln Thr Ser	
50 55 60	
atc ata aac cgg acc tct gtg ggg agc ttg cag gga ctg gct gtg gac	240

-87-

Ile 65	Ile	Asn	Arg	Thr	Ser 70	Val	Gly	Ser	Leu	Gln 75	Gly	Leu	Ala	Val	Asp 80	
atg	gac	tct	gtg	gta	cta	aat	gct	ggg	ctt	cgg	tca	gat	tac	tcg	tca	288
Met	Asp	Ser	Val	Val	Leu	Asn	Ala	Gly	Leu	Arg	Ser	Asp	Tyr	Ser	Ser	
				85					90					95		
acc	ata	gga	tct	gac	aaa	ggc	tgc	tct	cag	tac	ttc	tat	gca	gag	cat	336
Thr	Ile	Gly	Ser	Asp	Lys	Gly	Cys	Ser	Gln	Tyr	Phe	Tyr	Ala	Glu	His	
			100					105					110			
ctg	tct	ctc	cac	tac	ccg	ctg	gag	att	tct	gca	gcc	tca	ggg	agg	ctg	384
Leu	Ser	Leu	His	Tyr	Pro	Leu	Glu	Ile	Ser	Ala	Ala	Ser	Gly	Arg	Leu	
			115				120					125				
atg	tgt	cac	ttc	aag	ctg	gtg	gcc	ata	gtg	ggc	tac	ctg	att	cgt	ctc	432
Met	Cys	His	Phe	Lys	Leu	Val	Ala	Ile	Val	Gly	Tyr	Leu	Ile	Arg	Leu	
	130					135					140					
tca	atc	aag	tcc	atc	caa	atc	gaa	gcc	gac	aac	tgt	gtc	act	gac	tcc	480
Ser	Ile	Lys	Ser	Ile	Gln	Ile	Glu	Ala	Asp	Asn	Cys	Val	Thr	Asp	Ser	
145					150					155					160	
ctg	acc	att	tac	gac	tcc	ctt	ttg	ccc	atc	cgg	agc	agc	atc	ttg	tac	528
Leu	Thr	Ile	Tyr	Asp	Ser	Leu	Leu	Pro	Ile	Arg	Ser	Ser	Ile	Leu	Tyr	
				165					170					175		
aga	att	tgt	gaa	ccc	aca	aga	aca	tta	atg	tca	ttt	gtt	tct	aca	aat	576
Arg	Ile	Cys	Glu	Pro	Thr	Arg	Thr	Leu	Met	Ser	Phe	Val	Ser	Thr	Asn	
			180					185					190			
aat	ctc	atg	ttg	gtg	aca	ttt	aag	tct	cct	cat	ata	cgg	agg	ctc	tca	624
Asn	Leu	Met	Leu	Val	Thr	Phe	Lys	Ser	Pro	His	Ile	Arg	Arg	Leu	Ser	
		195					200					205				
gga	atc	cgg	gca	tat	ttt	gag	gtc	att	cca	gaa	caa	aag	tgt	gaa	aac	672
Gly	Ile	Arg	Ala	Tyr	Phe	Glu	Val	Ile	Pro	Glu	Gln	Lys	Cys	Glu	Asn	
	210					215					220					
aca	gtg	ttg	gtc	aaa	gac	atc	act	ggc	ttt	gaa	ggg	aaa	att	tca	agc	720
Thr	Val	Leu	Val	Lys	Asp	Ile	Thr	Gly	Phe	Glu	Gly	Lys	Ile	Ser	Ser	
225					230					235					240	
cca	tat	tac	ccg	agc	tac	tat	cct	cca	aaa	tgc	aag	tgt	acc	tgg	aaa	768
Pro	Tyr	Tyr	Pro	Ser	Tyr	Tyr	Pro	Pro	Lys	Cys	Lys	Cys	Thr	Trp	Lys	
				245					250					255		
ttt	cag	act	tct	cta	tca	act	ctt	ggc	ata	gca	ctg	aaa	ttc	tat	aac	816
Phe	Gln	Thr	Ser	Leu	Ser	Thr	Leu	Gly	Ile	Ala	Leu	Lys	Phe	Tyr	Asn	
			260					265					270			
tat	tca	ata	acc	aag	aag	agt	atg	aaa	ggc	tgt	gag	cat	gga	tgg	tgg	864
Tyr	Ser	Ile	Thr	Lys	Lys	Ser	Met	Lys	Gly	Cys	Glu	His	Gly	Trp	Trp	
		275					280					285				
gaa	att	tat	gag	cac	atg	tac	tgt	ggc	tcc	tac	atg	gat	cat	cag	aca	912
Glu	Ile	Tyr	Glu	His	Met	Tyr	Cys	Gly	Ser	Tyr	Met	Asp	His	Gln	Thr	
	290					295					300					
att	ttt	cga	gtg	ccc	agc	cct	ctg	gtt	cac	att	cag	ctc	cag	tgc	agt	960
Ile	Phe	Arg	Val	Pro	Ser	Pro	Leu	Val	His	Ile	Gln	Leu	Gln	Cys	Ser	

-88-

305	310	315	320	
tca agg ctt tca ggc aag cca ctt ttg gca gaa tat ggc agt tac aac Ser Arg Leu Ser Gly Lys Pro Leu Leu Ala Glu Tyr Gly Ser Tyr Asn 325 330 335				1008
atc agt caa ccc tgc cct gtg gga tct ttt aga tgc tcc tcc ggt tta Ile Ser Gln Pro Cys Pro Val Gly Ser Phe Arg Cys Ser Ser Gly Leu 340 345 350				1056
tgt gtc cct cag gcc cag cgt ggt gat gga gta aat gac tgc ttt gat Cys Val Pro Gln Ala Gln Arg Gly Asp Gly Val Asn Asp Cys Phe Asp 355 360 365				1104
gaa agt gat gaa ctg ttt tgc gtg agc cct caa cct gcc tgc aat acc Glu Ser Asp Glu Leu Phe Cys Val Ser Pro Gln Pro Ala Cys Asn Thr 370 375 380				1152
agc tcc ttc agg cag cat ggc cct ctc atc tgt gat ggc ttc agg gac Ser Ser Phe Arg Gln His Gly Pro Leu Ile Cys Asp Gly Phe Arg Asp 385 390 395 400				1200
tgt gag aat ggc cgg gat gag caa aac tgc act caa agt att cca tgc Cys Glu Asn Gly Arg Asp Glu Gln Asn Cys Thr Gln Ser Ile Pro Cys 405 410 415				1248
aac aac aga act ttt aag tgt ggc aat gat att tgc ttt agg aaa caa Asn Asn Arg Thr Phe Lys Cys Gly Asn Asp Ile Cys Phe Arg Lys Gln 420 425 430				1296
aat gca aaa tgt gat ggg aca gtg gat tgt cca gat gga agt gat gaa Asn Ala Lys Cys Asp Gly Thr Val Asp Cys Pro Asp Gly Ser Asp Glu 435 440 445				1344
gaa ggc tgc acc tgc agc agg agt tcc tcc gcc ctt cac cgc atc atc Glu Gly Cys Thr Cys Ser Arg Ser Ser Ser Ala Leu His Arg Ile Ile 450 455 460				1392
gga ggc aca gac acc ctg gag ggg ggt tgg ccg tgg cag gtc agc ctc Gly Gly Thr Asp Thr Leu Glu Gly Gly Trp Pro Trp Gln Val Ser Leu 465 470 475 480				1440
cac ttt gtt gga tct gcc tac tgt ggt gcc tca gtc atc tcc agg gag His Phe Val Gly Ser Ala Tyr Cys Gly Ala Ser Val Ile Ser Arg Glu 485 490 495				1488
tgg ctt ctt tct gca gcc cac tgt ttt cat gga aac agg ctg tca gat Trp Leu Leu Ser Ala Ala His Cys Phe His Gly Asn Arg Leu Ser Asp 500 505 510				1536
ccc aca cca tgg act gca cac ctc ggg atg tat gtt cag ggg aat gcc Pro Thr Pro Trp Thr Ala His Leu Gly Met Tyr Val Gln Gly Asn Ala 515 520 525				1584
aag ttt gtc tcc ccg gtg aga aga att gtg gtc cac gag tac tat aac Lys Phe Val Ser Pro Val Arg Arg Ile Val Val His Glu Tyr Tyr Asn 530 535 540				1632
agt cag act ttt gat tat gat att gct ttg cta cag ctc agt att gcc Ser Gln Thr Phe Asp Tyr Asp Ile Ala Leu Leu Gln Leu Ser Ile Ala 545 550 555 560				1680

-89-

tgg cct gag acc ctg aaa cag ctc att cag cca ata tgc att cct ccc	1728
Trp Pro Glu Thr Leu Lys Gln Leu Ile Gln Pro Ile Cys Ile Pro Pro	
565 570 575	
act ggt cag aga gtt cgc agt ggg gag aag tgc tgg gta act ggc tgg	1776
Thr Gly Gln Arg Val Arg Ser Gly Glu Lys Cys Trp Val Thr Gly Trp	
580 585 590	
ggg cga aga cac gaa gca gat aat aaa ggc tcc ctc gtt ctg cag caa	1824
Gly Arg Arg His Glu Ala Asp Asn Lys Gly Ser Leu Val Leu Gln Gln	
595 600 605	
gcg gag gta gag ctc att gat caa acg ctc tgt gtt tcc acc tac ggg	1872
Ala Glu Val Glu Leu Ile Asp Gln Thr Leu Cys Val Ser Thr Tyr Gly	
610 615 620	
atc atc act tct cgg atg ctc tgt gca ggc ata atg tca ggc aag aga	1920
Ile Ile Thr Ser Arg Met Leu Cys Ala Gly Ile Met Ser Gly Lys Arg	
625 630 635 640	
gat gcc tgc aaa gga gat tcg ggt gga cct tta tct tgt cga aga aaa	1968
Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Ser Cys Arg Arg Lys	
645 650 655	
agt gat gga aaa tgg att ttg act ggc att gtt agc tgg gga cat gga	2016
Ser Asp Gly Lys Trp Ile Leu Thr Gly Ile Val Ser Trp Gly His Gly	
660 665 670	
tgt gga cga cca aac ttt cct ggt gtt tac aca agg gtg tca aac ttt	2064
Cys Gly Arg Pro Asn Phe Pro Gly Val Tyr Thr Arg Val Ser Asn Phe	
675 680 685	
gtt ccc tgg att cat aaa tat gtc cct tct ctt ttg taa t tgcaaaaaaa	2114
Val Pro Trp Ile His Lys Tyr Val Pro Ser Leu Leu *	
690 695 700	

aaaaaaaaaaaa

2130

<210> 45

<211> 700

<212> PRT

<213> Homo Sapien

<400> 45

Ile Asn Leu Val Tyr Thr Thr Ser Ala Phe Ser Lys Phe Tyr Glu Gln	
1 5 10 15	
Ser Val Val Ala Asp Val Ser Ser Asn Asn Lys Gly Gly Leu Leu Val	
20 25 30	
His Phe Trp Ile Val Phe Val Met Pro Arg Ala Lys Gly His Ile Phe	
35 40 45	
Cys Glu Asp Cys Val Ala Ala Ile Leu Lys Asp Ser Ile Gln Thr Ser	
50 55 60	
Ile Ile Asn Arg Thr Ser Val Gly Ser Leu Gln Gly Leu Ala Val Asp	
65 70 75 80	
Met Asp Ser Val Val Leu Asn Ala Gly Leu Arg Ser Asp Tyr Ser Ser	
85 90 95	
Thr Ile Gly Ser Asp Lys Gly Cys Ser Gln Tyr Phe Tyr Ala Glu His	
100 105 110	
Leu Ser Leu His Tyr Pro Leu Glu Ile Ser Ala Ala Ser Gly Arg Leu	
115 120 125	

-90-

Met	Cys	His	Phe	Lys	Leu	Val	Ala	Ile	Val	Gly	Tyr	Leu	Ile	Arg	Leu
130						135					140				
Ser	Ile	Lys	Ser	Ile	Gln	Ile	Glu	Ala	Asp	Asn	Cys	Val	Thr	Asp	Ser
145					150					155					160
Leu	Thr	Ile	Tyr	Asp	Ser	Leu	Leu	Pro	Ile	Arg	Ser	Ser	Ile	Leu	Tyr
				165					170					175	
Arg	Ile	Cys	Glu	Pro	Thr	Arg	Thr	Leu	Met	Ser	Phe	Val	Ser	Thr	Asn
			180					185					190		
Asn	Leu	Met	Leu	Val	Thr	Phe	Lys	Ser	Pro	His	Ile	Arg	Arg	Leu	Ser
		195					200					205			
Gly	Ile	Arg	Ala	Tyr	Phe	Glu	Val	Ile	Pro	Glu	Gln	Lys	Cys	Glu	Asn
210					215						220				
Thr	Val	Leu	Val	Lys	Asp	Ile	Thr	Gly	Phe	Glu	Gly	Lys	Ile	Ser	Ser
225					230					235					240
Pro	Tyr	Tyr	Pro	Ser	Tyr	Tyr	Pro	Pro	Lys	Cys	Lys	Cys	Thr	Trp	Lys
				245					250					255	
Phe	Gln	Thr	Ser	Leu	Ser	Thr	Leu	Gly	Ile	Ala	Leu	Lys	Phe	Tyr	Asn
			260				265						270		
Tyr	Ser	Ile	Thr	Lys	Lys	Ser	Met	Lys	Gly	Cys	Glu	His	Gly	Trp	Trp
		275					280					285			
Glu	Ile	Tyr	Glu	His	Met	Tyr	Cys	Gly	Ser	Tyr	Met	Asp	His	Gln	Thr
290					295						300				
Ile	Phe	Arg	Val	Pro	Ser	Pro	Leu	Val	His	Ile	Gln	Leu	Gln	Cys	Ser
305					310					315					320
Ser	Arg	Leu	Ser	Gly	Lys	Pro	Leu	Leu	Ala	Glu	Tyr	Gly	Ser	Tyr	Asn
				325					330					335	
Ile	Ser	Gln	Pro	Cys	Pro	Val	Gly	Ser	Phe	Arg	Cys	Ser	Ser	Gly	Leu
			340				345						350		
Cys	Val	Pro	Gln	Ala	Gln	Arg	Gly	Asp	Gly	Val	Asn	Asp	Cys	Phe	Asp
		355					360				365				
Glu	Ser	Asp	Glu	Leu	Phe	Cys	Val	Ser	Pro	Gln	Pro	Ala	Cys	Asn	Thr
370					375						380				
Ser	Ser	Phe	Arg	Gln	His	Gly	Pro	Leu	Ile	Cys	Asp	Gly	Phe	Arg	Asp
385					390					395					400
Cys	Glu	Asn	Gly	Arg	Asp	Glu	Gln	Asn	Cys	Thr	Gln	Ser	Ile	Pro	Cys
				405					410					415	
Asn	Asn	Arg	Thr	Phe	Lys	Cys	Gly	Asn	Asp	Ile	Cys	Phe	Arg	Lys	Gln
			420				425						430		
Asn	Ala	Lys	Cys	Asp	Gly	Thr	Val	Asp	Cys	Pro	Asp	Gly	Ser	Asp	Glu
		435					440					445			
Glu	Gly	Cys	Thr	Cys	Ser	Arg	Ser	Ser	Ser	Ala	Leu	His	Arg	Ile	Ile
450					455						460				
Gly	Gly	Thr	Asp	Thr	Leu	Glu	Gly	Gly	Trp	Pro	Trp	Gln	Val	Ser	Leu
465					470					475					480
His	Phe	Val	Gly	Ser	Ala	Tyr	Cys	Gly	Ala	Ser	Val	Ile	Ser	Arg	Glu
				485					490					495	
Trp	Leu	Leu	Ser	Ala	Ala	His	Cys	Phe	His	Gly	Asn	Arg	Leu	Ser	Asp
			500					505					510		
Pro	Thr	Pro	Trp	Thr	Ala	His	Leu	Gly	Met	Tyr	Val	Gln	Gly	Asn	Ala
		515					520					525			
Lys	Phe	Val	Ser	Pro	Val	Arg	Arg	Ile	Val	Val	His	Glu	Tyr	Tyr	Asn
		530				535					540				
Ser	Gln	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Ser	Ile	Ala
545					550					555					560
Trp	Pro	Glu	Thr	Leu	Lys	Gln	Leu	Ile	Gln	Pro	Ile	Cys	Ile	Pro	Pro
				565					570					575	
Thr	Gly	Gln	Arg	Val	Arg	Ser	Gly	Glu	Lys	Cys	Trp	Val	Thr	Gly	Trp
			580				585						590		
Gly	Arg	Arg	His	Glu	Ala	Asp	Asn	Lys	Gly	Ser	Leu	Val	Leu	Gln	Gln
		595					600					605			
Ala	Glu	Val	Glu	Leu	Ile	Asp	Gln	Thr	Leu	Cys	Val	Ser	Thr	Tyr	Gly

-91-

610		615		620											
Ile	Ile	Thr	Ser	Arg	Met	Leu	Cys	Ala	Gly	Ile	Met	Ser	Gly	Lys	Arg
625					630					635					640
Asp	Ala	Cys	Lys	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ser	Cys	Arg	Arg	Lys
				645					650						655
Ser	Asp	Gly	Lys	Trp	Ile	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	His	Gly
			660					665					670		
Cys	Gly	Arg	Pro	Asn	Phe	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	Asn	Phe
		675				680						685			
Val	Pro	Trp	Ile	His	Lys	Tyr	Val	Pro	Ser	Leu	Leu				
	690				695						700				

<210> 46
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Conjugate

<221> MOD_RES
 <222> 1

<221> MOD_RES
 <222> 4
 <223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
 <222> 8
 <223> Alanine-therapeutic agent

<400> 46
 Leu Arg Ala Xaa Gly Arg Ala Xaa
 1 5

<210> 47
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Conjugate

<221> ACETYLTATION
 <222> 1

<221> MOD_RES
 <222> 4
 <223> Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
 <222> 8
 <223> Xaa is Alanine-therapeutic agent

<400> 47
 Leu Arg Ala Xaa Ala Arg Ala Xaa
 1 5

<210> 48
 <211> 8
 <212> PRT

-92-

<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 48
Leu Arg Ser Xaa Gly Arg Ala Xaa
1 5

<210> 49
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 49
Leu Arg Ser Xaa Ala Arg Ala Xaa
1 5

<210> 50
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 50
Leu Arg Pro Arg Phe Lys Ile Xaa
1 5

-93-

<210> 51
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Isoleucine-therapeutic agent

<400> 51
Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 52
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 52
Pro Arg Phe Lys Ile Xaa
1 5

<210> 53
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 53
Leu Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 54
<211> 7
<212> PRT
<213> Artificial sequence

-94-

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 54
Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 55
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 55
Ser Lys Ser Arg Ala Xaa
1 5

<210> 56
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 56
Leu Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 57
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION

-95-

<222> 1
<221> MOD_RES
<222> 7
<223> Isoleucine-therapeutic agent

<400> 57
Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 58
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 58
Pro Arg Phe Arg Ile Xaa
1 5

<210> 59
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 59
Leu Arg Ser Arg Ser Arg Ala Xaa
1 5

<210> 60
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7

-96-

<223> Alanine-therapeutic agent

<400> 60

Arg Ser Arg Ser Arg Ala Xaa
1 5

<210> 61

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 61

Ser Arg Ser Arg Ala Xaa
1 5

<210> 62

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 62

Leu Arg Ala Xaa Gly Arg Ala Xaa
1 5

<210> 63

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

-97-

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 63

Leu Arg Ala Xaa Ala Arg Ala Xaa
1 5

<210> 64

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 64

Leu Arg Ser Xaa Gly Arg Ala Xaa
1 5

<210> 65

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat:
(R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 65

Leu Arg Ser Xaa Ala Arg Ala Xaa
1 5

<210> 66

<211> 8

<212> PRT

<213> Artificial sequence

-98-

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 66
Leu Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 67
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Isoleucine-therapeutic agent

<400> 67
Arg Pro Arg Phe Lys Ile Xaa
1 5

<210> 68
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 68
Pro Arg Phe Lys Ile Xaa
1 5

<210> 69
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION

-99-

<222> 1
<221> MOD_RES
<222> 8
<223> Alanine-therapeutic agent

<400> 69
Leu Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 70
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 70
Arg Ser Lys Ser Arg Ala Xaa
1 5

<210> 71
<211> 6
<212> PRT
<213> Artifical sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (1)...(0)

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 71
Ser Lys Ser Arg Ala Xaa
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8

-100-

<223> Isoleucine-therapeutic agent

<400> 72

Leu Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 73

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Isoleucine-therapeutic agent

<400> 73

Arg Pro Arg Phe Arg Ile Xaa
1 5

<210> 74

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Isoleucine-therapeutic agent

<400> 74

Pro Arg Phe Arg Ile Xaa
1 5

<210> 75

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-Therapeutic Agent

<400> 75

Leu Arg Ser Arg Ser Arg Ala Xaa

-101-

1 5

<210> 76
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 76
Arg Ser Arg Ser Arg Ala Xaa
1 5

<210> 77
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 77
Ser Arg Ser Arg Ala Xaa
1 5

<210> 78
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 78
Xaa Pro Arg Ala Xaa
1 5

<210> 79

-102-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT:
HHT is hexahydrotyrosol

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 79
Xaa Gly Arg Ala Xaa
1 5

<210> 80
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-p-tosyl-Gly

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 80
Xaa Pro Arg Ala Xaa
1 5

<210> 81
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 81
Xaa Gly Arg Ala Xaa
1 5

<210> 82

-103-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 82
Xaa Gly Arg Ala Xaa
1 5

<210> 83
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 83
Xaa Gly Arg Ala Xaa
1 5

<210> 84
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 84
Xaa Gly Arg Ala Xaa
1 5

-104-

<210> 85
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES
<222> 5
<223> Alanine- therapeutic agent

<400> 85
Xaa Pro Arg Ala Xaa
1 5

<210> 86
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO):
Cbo is carbobenzoxy

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 86
Xaa Arg Ala Ala Xaa
1 5

<210> 87
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 87
Xaa Phe Arg Ala Xaa
1 5

-105-

<210> 88
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MUTAGEN
<222> 5
<223> Alanine-therapeutic agent

<400> 88
Xaa Leu Arg Ala Xaa
1 5

<210> 89
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile:
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 89
Xaa Glu Gly Arg Ala Xaa
1 5

<210> 90
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile:
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 90
Xaa Xaa Gly Arg Ala Xaa
1 5

-106-

<210> 91
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Pro

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 91
Xaa Phe Arg Ala Xaa
1 5

<210> 92
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> pipecolinic acid

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 92
Xaa Xaa Arg Ala Xaa
1 5

<210> 93
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 93

-107-

Xaa Leu Lys Ala Xaa
1 5

<210> 94
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Nle

<221> MOD_RES
<222> 2
<223> HHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 94
Xaa Xaa Lys Ala Xaa
1 5

<210> 95
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 95
Xaa Arg Thr Lys Arg Ala Xaa
1 5

<210> 96
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-Arg

<221> MOD_RES

-108-

<222> 6
<223> Alanine-therapeutic agent

<400> 96
Xaa Gln Arg Arg Ala Xaa
1 5

<210> 97
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Boc-Gln:
Boc is t-butoxycarbonyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 97
Xaa Gly Arg Ala Xaa
1 5

<210> 98
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Z-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 4
<223> Alanine-therapeutic agent

<400> 98
Xaa Arg Ala Xaa
1

<210> 99
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-HHT: HHT is hexahydrotyrosol

-109-

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 99
Xaa Ala Arg Ala Xaa
1 5

<210> 100
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-CHT:
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 100
Xaa Gly Arg Ala Xaa
1 5

<210> 101
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is MeSO₂-D-Phe

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 101
Xaa Pro Arg Ala Xaa
1 5

<210> 102
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1

-110-

<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 102

Xaa Pro Arg Ala Xaa

1 5

<210> 103

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is CH₃SO₂-D-CHA:

CHA is cyclohexylalanyl

<221> MOD_RES

<222> 2

<223> Xaa is But-Arg

<221> MOD_RES

<222> 4

<223> Alanine-therapeutic agent

<400> 103

Xaa Xaa Ala Xaa

1

<210> 104

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 104

Arg Gln Ser Arg Ala Xaa

1 5

<210> 105

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

-111-

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Ala-therapeutic agent

<400> 105

Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 106

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 106

Leu Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 107

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 107

Arg Gln Ser Arg Xaa
1 5

<210> 108

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<221> MOD_RES

-112-

<222> 6
<223> Alanine-therapeutic agent

<400> 108
Arg Arg Gln Ser Arg Xaa
1 5

<210> 109
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Glycine-therapeutic agent

<400> 109
Leu Arg Arg Gln Ser Arg Gly Xaa
1 5

<210> 110
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 110
Leu Arg Arg Gln Ser Arg Xaa
1 5

<210> 111
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 111

-113-

Arg Arg Gln Ser Arg Xaa
1 5

<210> 112
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Isoleucine-therapeutic agent

<400> 112
Leu Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (1)...(0)

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(Alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 113
Leu Arg Ala Xaa Gly Arg Ser Xaa
1 5

<210> 114
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

-114-

<222> 8
<223> Leucine-therapeutic agent

<400> 114
Leu Arg Ala Xaa Ala Arg Ser Xaa
1 5

<210> 115
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 115
Leu Arg Ser Xaa Gly Arg Ser Xaa
1 5

<210> 116
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 116
Leu Arg Ser Xaa Ala Arg Ser Xaa
1 5

<210> 117
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-115-

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 117

Leu Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 118

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 118

Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 119

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 119

Pro Arg Phe Lys Ser Xaa
1 5

<210> 120

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

-116-

<222> 8
<223> Leucine-therapeutic agent

<400> 120
Leu Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 121
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 121
Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 122
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 122
Ser Lys Ser Arg Ser Xaa
1 5

<210> 123
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 123

-117-

Leu Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 124
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 124
Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 125
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 125
Pro Arg Phe Arg Ser Xaa
1 5

<210> 126
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 126
Leu Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 127

-118-

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 127
Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 128
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 128
Ser Arg Ser Arg Ser Xaa
1 5

<210> 129
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 129
Leu Arg Ala Xaa Gly Arg Ser Xaa
1 5

<210> 130

-119-

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 130
Leu Arg Ala Xaa Ala Arg Ser Xaa
1 5

<210> 131
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 131
Leu Arg Ser Xaa Gly Arg Ser Xaa
1 5

<210> 132
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

-120-

<222> 8
<223> Leucine-therapeutic agent

<400> 132
Leu Arg Ser Xaa Ala Arg Ser Xaa
1 5

<210> 133
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 133
Leu Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 134
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 134
Arg Pro Arg Phe Lys Ser Xaa
1 5

<210> 135
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 135

-121-

Pro Arg Phe Lys Ser Xaa
1 5

<210> 136
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 136
Leu Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 137
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 137
Arg Ser Lys Ser Arg Ser Xaa
1 5

<210> 138
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 138
Ser Lys Ser Arg Ser Xaa
1 5

<210> 139

-122-

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 139
Leu Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 140
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 140
Arg Pro Arg Phe Arg Ser Xaa
1 5

<210> 141
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 141
Pro Arg Phe Arg Ser Xaa
1 5

<210> 142
<211> 8
<212> PRT
<213> Artificial Sequence

-123-

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 142
Leu Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 143
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 143
Arg Ser Arg Ser Arg Ser Xaa
1 5

<210> 144
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 144
Ser Arg Ser Arg Ser Xaa
1 5

<210> 145
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES

-124-

<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 145
Xaa Pro Arg Ser Xaa
1 5

<210> 146
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 146
Xaa Gly Arg Ser Xaa
1 5

<210> 147
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is n-p-tosyl-Gly

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 147
Xaa Pro Arg Ser Xaa
1 5

<210> 148
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> MOD_RES

-125-

<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 148
Xaa Gly Arg Ser Xaa
1 5

<210> 149
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 149
Xaa Gly Arg Ser Xaa
1 5

<210> 150
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg;
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 150
Xaa Gly Arg Ser Xaa
1 5

<210> 151
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-126-

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 151
Xaa Gly Arg Ser Xaa
1 5

<210> 152
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 152
Xaa Pro Arg Ser Xaa
1 5

<210> 153
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO);
Cbo is carbobenzoxy

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 153
Xaa Gly Arg Ser Xaa
1 5

<210> 154
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-127-

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 154
Xaa Phe Arg Ser Xaa
1 5

<210> 155
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 155
Xaa Leu Arg Ser Xaa
1 5

<210> 156
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile;
Bz is benzoyl

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 156
Xaa Glu Gly Arg Ser Xaa
1 5

<210> 157
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

-128-

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile

<221> MOD_RES
<222> 2
<223> Xaa is Glu(gamma-OMe)

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 157
Xaa Xaa Gly Arg Ser Xaa
1 5

<210> 158
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is benzoyl-Pro

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 158
Xaa Phe Arg Ser Xaa
1 5

<210> 159
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> Xaa is Pip is pipercolinic acid

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic acid

<400> 159
Xaa Xaa Arg Ser Xaa
1 5

<210> 160

-129-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic acid

<400> 160
Xaa Leu Lys Ser Xaa
1 5

<210> 161
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Nle

<221> MOD_RES
<222> 2
<223> Xaa is HHT: hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Xaa is leucine-therapeutic agent

<400> 161
Xaa Xaa Lys Ser Xaa
1 5

<210> 162
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 162
Xaa Arg Thr Lys Arg Ser Xaa

-130-

1 5

<210> 163
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-Arg

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 163
Xaa Gln Arg Arg Ser Xaa
1 5

<210> 164
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Boc-Gln

<221> MOD_RES
<222> 5
<223> Xaa is Leucine-therapeutic agent

<400> 164
Xaa Gly Arg Ser Xaa
1 5

<210> 165
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Z-Arg:
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 4
<223> Leucine-therapeutic agent

<400> 165
Xaa Arg Ser Xaa

-131-

1

<210> 166
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-HHT: HHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 166
Xaa Ala Arg Ser Xaa
1 5

<210> 167
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-CHT: CHT is hexahydrotyrosyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 167
Xaa Gly Arg Ser Xaa
1 5

<210> 168
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is MeSO₂-dPhe

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 168
Xaa Pro Arg Ser Xaa
1 5

-132-

<210> 169
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 169
Xaa Pro Arg Ser Xaa
1 5

<210> 170
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-CHA: CHA is cyclohexylalanyl

<221> MOD_RES
<222> 2
<223> Xaa is But-Arg

<221> MOD_RES
<222> 4
<223> Leucine-therapeutic agent

<400> 170
Xaa Xaa Ser Xaa
1

<210> 171
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 171

-133-

Arg Gln Ser Arg Ser Xaa
1 5

<210> 172
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 172
Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 173
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 173
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 174
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 174
Arg Gln Ser Arg Xaa
1 5

<210> 175

-134-

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 175
Arg Arg Gln Ser Arg Xaa
1 5

<210> 176
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 176
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 177
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 177
Leu Arg Arg Gln Ser Arg Xaa
1 5

<210> 178
<211> 6
<212> PRT
<213> Artificial Sequence

-135-

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 178
Arg Arg Gln Ser Arg Xaa
1 5

<210> 179
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 179
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 180
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 180
Arg Gln Gly Arg Ser Xaa
1 5

<210> 181
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION

-136-

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 181

Arg Gln Ala Arg Ser Xaa
1 5

<210> 182

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 182

Arg Gln Phe Arg Ser Xaa
1 5

<210> 183

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 183

Arg Ser Arg Ser Xaa
1 5

<210> 184

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

-137-

<223> Leucine-therapeutic agent

<400> 184

Arg Gly Arg Ser Xaa
1 5

<210> 185

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 185

Arg Ala Arg Ser Xaa
1 5

<210> 186

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 186

Arg Phe Arg Ser Xaa
1 5

<210> 187

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 187

Gln Ser Arg Ser Xaa

-138-

1	5
---	---

<210> 188
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 188
Gln Gly Arg Ser Xaa
1 5

<210> 189
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 189
Gln Ala Arg Ser Xaa
1 5

<210> 190
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 190
Gln Phe Arg Ser Xaa
1 5

<210> 191
<211> 9

-139-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(Alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 191
Leu Arg Ala Xaa Gly Arg Ser Ser Xaa
1 5

<210> 192
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 192
Leu Arg Ala Xaa Ala Arg Ser Ser Xaa
1 5

<210> 193
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9

-140-

<223> Leucine-therapeutic agent

<400> 193

Leu Arg Ser Xaa Gly Arg Ser Ser Xaa
1 5

<210> 194

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 194

Leu Arg Ser Xaa Ala Arg Ser Ser Xaa
1 5

<210> 195

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 195

Leu Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 196

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

-141-

<223> Leucine-therapeutic agent

<400> 196

Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 197

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 197

Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 198

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 198

Leu Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 199

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 199

Arg Ser Lys Ser Arg Ser Ser Xaa

-142-

1 5

<210> 200
<211> 7
<212> PRT
<213> Aritificial sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 200
Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 201
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 201
Leu Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 202
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 202
Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 203
<211> 7

-143-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 203
Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 204
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 204
Leu Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 205
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 205
Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 206
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

-144-

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 206

Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 207

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> (0)...(0)

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 207

Leu Arg Ala Xaa Gly Arg Ser Ser Xaa
1 5

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 208

Leu Arg Ala Xaa Ala Arg Ser Ser Xaa
1 5

<210> 209

<211> 9

-145-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 209
Leu Arg Ser Xaa Gly Arg Ser Ser Xaa
1 5

<210> 210
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Quat: (R)-Glu(alpha-(3-amidinobenzyl))

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 210
Leu Arg Ser Xaa Ala Arg Ser Ser Xaa
1 5

<210> 211
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 211
Leu Arg Pro Arg Phe Lys Ser Ser Xaa

-146-

1 5

<210> 212
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 212
Arg Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 213
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 213
Pro Arg Phe Lys Ser Ser Xaa
1 5

<210> 214
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 214
Leu Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 215
<211> 8

-147-

<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 215
Arg Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 216
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 216
Ser Lys Ser Arg Ser Ser Xaa
1 5

<210> 217
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 217
Leu Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 218
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

-148-

<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 218
Arg Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 219
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 219
Pro Arg Phe Arg Ser Ser Xaa
1 5

<210> 220
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 220
Leu Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 221
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

-149-

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 221
Arg Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 222
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 222
Ser Arg Ser Arg Ser Ser Xaa
1 5

<210> 223
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 223
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 224
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES

-150-

<222> 6
<223> Leucine-therapeutic agent

<400> 224
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 225
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is n-p-tosyl-Gly

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 225
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 226
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Benzoyl-Val

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 226
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 227
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH₃SO₂-D-HHT;
HHT is hexahydrotyrosyl

<221> MOD_RES

-151-

<222> 6
<223> Leucine-therapeutic agent

<400> 227
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 228
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-alpha-Z-D-Arg;
Z is benzyloxycarbonyl

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 228
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 229
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is pyroglutamic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 229
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 230
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Ile

<221> MOD_RES

-152-

<222> 6
<223> Leucine-therapeutic agent

<400> 230
Xaa Pro Arg Ser Ser Xaa
1 5

<210> 231
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Cbo-L-(gamma)Glu(alpha-t-BuO);
Cbo is carbobenzoxy

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 231
Xaa Gly Arg Ser Ser Xaa
1 5

<210> 232
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Pro

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 232
Xaa Phe Arg Ser Ser Xaa
1 5

<210> 233
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES

-153-

<222> 6
<223> Leucine-therapeutic agent

<400> 233
Xaa Leu Arg Ser Ser Xaa
1 5

<210> 234
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile;
Bz is benzoyl

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 234
Xaa Glu Gly Arg Ser Ser Xaa
1 5

<210> 235
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Bz-Ile

<221> MOD_RES
<222> 2
<223> Xaa is Glu(gamma-OMe)

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 235
Xaa Xaa Gly Arg Ser Ser Xaa
1 5

<210> 236
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES

-154-

<222> 1
<223> Xaa is benzoyle-Pro

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 236
Xaa Phe Arg Ser Ser Xaa
1 5

<210> 237
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Phe

<221> MOD_RES
<222> 2
<223> Xaa is Pip is pipercolinic acid

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic acid

<400> 237
Xaa Xaa Arg Ser Ser Xaa
1 5

<210> 238
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is H-D-Val

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic acid

<400> 238
Xaa Leu Lys Ser Ser Xaa
1 5

<210> 239
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

-155-

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-Nle

<221> MOD_RES

<222> 2

<223> Xaa is HHT: hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Xaa is leucine-therapeutic agent

<400> 239

Xaa Xaa Lys Ser Ser Xaa

1

5

<210> 240

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is pyroglutamic acid

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 240

Xaa Arg Thr Lys Arg Ser Ser Xaa

1

5

<210> 241

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-Arg

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<400> 241

Xaa Gln Arg Arg Ser Ser Xaa

1

5

<210> 242

<211> 6

<212> PRT

-156-

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Boc-Gln

<221> MOD_RES

<222> 6

<223> Xaa is Leucine-therapeutic agent

<400> 242

Xaa Gly Arg Ser Ser Xaa

1

5

<210> 243

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Z-Arg:

Z is benzyloxycarbonyl

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 243

Xaa Arg Ser Ser Xaa

1

5

<210> 244

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-HHT: HHT is hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 244

Xaa Ala Arg Ser Ser Xaa

1

5

<210> 245

<211> 6

<212> PRT

-157-

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is H-D-CHT: CHT is hexahydrotyrosyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 245

Xaa Gly Arg Ser Ser Xaa

1

5

<210> 246

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is MeSO₂-dPhe

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 246

Xaa Pro Arg Ser Ser Xaa

1

5

<210> 247

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> MOD_RES

<222> 1

<223> Xaa is delta-Z-D-Lys: Z is benzyloxycarbonyl

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 247

Xaa Pro Arg Ser Ser Xaa

1

5

<210> 248

<211> 5

<212> PRT

<213> Artificial Sequence

-158-

<220>
<223> Conjugate

<221> MOD_RES
<222> 1
<223> Xaa is CH3SO2-D-CHA: CHA is cyclohexylalanyl

<221> MOD_RES
<222> 2
<223> Xaa is But-Arg

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 248
Xaa Xaa Ser Ser Xaa
1 5

<210> 249
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 249
Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 250
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 250
Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 251
<211> 9
<212> PRT

-159-

<213> Artificial sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 251

Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 252

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 252

Arg Gln Ser Arg Xaa
1 5

<210> 253

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 253

Arg Arg Gln Ser Arg Xaa
1 5

<210> 254

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Conjugate

-160-

<221> MOD_RES
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic agent

<400> 254
Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 255
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 255
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 256
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 256
Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 257
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES

-161-

<222> 9
<223> Leucine-therapeutic agent

<400> 257
Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 258
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 258
Arg Gln Gly Arg Ser Ser Xaa
1 5

<210> 259
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 259
Arg Gln Ala Arg Ser Ser Xaa
1 5

<210> 260
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic acid

<400> 260

-162-

Arg Gln Phe Arg Ser Ser Xaa
1 5

<210> 261
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 261
Arg Ser Arg Ser Ser Xaa
1 5

<210> 262
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 262
Arg Gly Arg Ser Ser Xaa
1 5

<210> 263
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 263
Arg Ala Arg Ser Ser Xaa
1 5

<210> 264

-163-

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 264
Arg Phe Arg Ser Ser Xaa
1 5

<210> 265
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 265
Gln Ser Arg Ser Ser Xaa
1 5

<210> 266
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 266
Gln Gly Arg Ser Ser Xaa
1 5

<210> 267
<211> 6
<212> PRT
<213> Artificial Sequence

-164-

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> leucine-therapeutic agent

<400> 267
Gln Ala Arg Ser Ser Xaa
1 5

<210> 268
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 268
Gln Phe Arg Ser Ser Xaa
1 5

<210> 269
<211> 816
<212> DNA
<213> Homo Sapien

<220>
<221> CDS
<222> (1)...(816)
<223> Nucleotide sequence encoding MTSP25, including
MTSP25 protease domain

<221> misc feature
<222> (248)...(270)
<223> Transmembrane domain encompasses amino acids
248-270 at the C-terminus of the trypsin-like
serine protease domain (amino acids 1-237)

<400> 269
att ata ggg ggc acc gaa gca caa gct ggc gca tgg ccg tgg gtg gtg 48
Ile Ile Gly Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val
1 5 10 15

agc ctg cag att aaa tat ggc cgt gtt ctt gtt cat gta tgt ggg gga 96
Ser Leu Gln Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly
20 25 30

acc cta gtg aga gag agg tgg gtc ctc aca gct gcc cac tgc act aaa 144
Thr Leu Val Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys

-165-

35	40	45	
gac gct agc gat cct tta atg tgg aca gct gtg att gga act aat aat			192
Asp Ala Ser Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn			
50	55	60	
ata cat gga cgc tat cct cat acc aag aag ata aaa att aaa gca atc			240
Ile His Gly Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile			
65	70	75	80
att att cat cca aac ttc att ttg gaa tct tat gta aat gat att gca			288
Ile Ile His Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala			
	85	90	95
ctt ttt cac tta aaa aaa gca gtg agg tat aat gac tat att cag cct			336
Leu Phe His Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro			
	100	105	110
att tgc cta cct ttt gat gtt ttc caa atc ctg gac gga aac aca aag			384
Ile Cys Leu Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys			
	115	120	125
tgt ttt ata agt ggc tgg gga aga aca aaa gaa gaa ggt aac gct aca			432
Cys Phe Ile Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala Thr			
	130	135	140
aat att tta caa gat gca gaa gtg cat tat att tct cga gag atg tgt			480
Asn Ile Leu Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys			
145	150	155	160
aat tct gag agg agt tat ggg gga ata att cct aac act tca ttt tgt			528
Asn Ser Glu Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys			
	165	170	175
gca ggt gat gaa gat gga gct ttt gat act tgc agg ggt gac agt ggg			576
Ala Gly Asp Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly			
	180	185	190
gga cca tta atg tgc tac tta cca gaa tat aaa aga ttt ttt gta atg			624
Gly Pro Leu Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met			
	195	200	205
gga att acc agt tac gga cat ggc tgt ggt cga aga ggt ttt cct ggt			672
Gly Ile Thr Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly			
	210	215	220
gtc tat att ggg cca tcc ttc tac caa aag tgg ctg aca gag cat ttc			720
Val Tyr Ile Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe			
225	230	235	240
ttc cat gca agc act caa ggc ata ctt act ata aat att tta cgt ggc			768
Phe His Ala Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly			
	245	250	255
cag atc ctc ata gct tta tgt ttt gtc atc tta cta gca aca aca taa			816
Gln Ile Leu Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr *			
	260	265	270

<210> 270

<211> 271

<212> PRT

-166-

<213> Homo Sapien

<400> 270

```

Ile Ile Gly Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val
 1           5           10           15
Ser Leu Gln Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly
          20           25           30
Thr Leu Val Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys
          35           40           45
Asp Ala Ser Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn
 50           55           60
Ile His Gly Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile
 65           70           75           80
Ile Ile His Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala
          85           90           95
Leu Phe His Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro
          100          105          110
Ile Cys Leu Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys
          115          120          125
Cys Phe Ile Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala Thr
          130          135          140
Asn Ile Leu Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys
 145          150          155          160
Asn Ser Glu Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys
          165          170          175
Ala Gly Asp Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly
          180          185          190
Gly Pro Leu Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met
          195          200          205
Gly Ile Thr Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly
 210          215          220
Val Tyr Ile Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe
 225          230          235          240
Phe His Ala Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly
          245          250          255
Gln Ile Leu Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr
          260          265          270

```

<210> 271

<211> 8

<212> PRT

<213> amino acids 401-407 of SEQ ID No. 97 in WO 02/00860

<400> 271

```

Arg Lys His Leu Pro Arg Pro Ala
 1           5

```

<210> 272

<211> 228

<212> PRT

<213> alternative PD1 of MTSP12

<400> 272

```

Ile Val Gly Gly Met Glu Ala Ser Pro Gly Glu Phe Pro Trp Gln Ala
 1           5           10           15
Ser Leu Arg Glu Asn Lys Glu His Phe Cys Gly Ala Ala Ile Ile Asn
          20           25           30
Ala Arg Trp Leu Val Ser Ala Ala His Cys Phe Asn Glu Phe Gln Asp
          35           40           45

```

-167-

```

Pro Thr Lys Trp Val Ala Tyr Val Gly Ala Thr Tyr Leu Ser Gly Ser
  50      55      60
Glu Ala Ser Thr Val Arg Ala Gln Val Val Gln Ile Val Lys His Pro
  65      70      75      80
Leu Tyr Asn Ala Asp Thr Ala Asp Phe Asp Val Ala Val Leu Glu Leu
      85      90      95
Thr Ser Pro Leu Pro Phe Gly Arg His Ile Gln Pro Val Cys Leu Pro
      100      105      110
Ala Ala Thr His Ile Phe Pro Pro Ser Lys Lys Cys Leu Ile Ser Gly
      115      120      125
Trp Gly Tyr Leu Lys Glu Asp Phe Leu Arg Lys His Leu Pro Arg Pro
      130      135      140
Ala Val Lys Pro Gly Val Leu Gln Lys Ala Thr Val Glu Leu Leu Asp
      145      150      155      160
Gln Ala Leu Cys Ala Ser Leu Tyr Gly His Ser Leu Thr Asp Arg Met
      165      170      175
Val Cys Ala Gly Tyr Leu Asp Gly Lys Val Asp Ser Cys Gln Gly Asp
      180      185      190
Ser Gly Gly Pro Leu Val Cys Glu Glu Pro Ser Gly Arg Phe Ser Leu
      195      200      205
Ala Gly Ile Val Ser Trp Gly Ile Gly Cys Ala Glu Ala Arg Arg Pro
      210      215      220
Gly Val Tyr Ala
      225

```

<210> 273

<211> 804

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(804)

<223> Nucleotide sequence encoding MTSP20, including
MTSP20 protease domain

<400> 273

```

aca gca ggt ccc cag gca gga gca ccc tcc cca tgg ccc tgg gag gcc      48
Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala
  1              5              10              15

agg ctg atg cac cag gga cag ctg gcc tgt ggc gga gcc ctg gtg tca      96
Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser
      20              25              30

gag gag acg gtg cta act gtt gcc cac tgc ttc att ggg cgc cag gcc      144
Glu Glu Thr Val Leu Thr Val Ala His Cys Phe Ile Gly Arg Gln Ala
      35              40              45

cca gag gaa tgg agc gta ggg ctg ggg acc aga ccg gag gag tgg ggc      192
Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly
      50              55              60

ctg aag cag ctc atc ctg cat gga gcc tac acc cac cct gag ggg ggc      240
Leu Lys Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly
      65              70              75              80

tac gac atg gcc ctc ctg ctg ctg gcc cag cct gtg aca ctg gga gcc      288
Tyr Asp Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala
      85              90              95

```

-168-

```

agc ctg cgg ccc ctc tgc ctg ccc tat cct gac cac cac ctg cct gat      336
Ser Leu Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp
          100                      105                      110

ggg gag cgt ggc tgg gtt ctg gga cgg gcc cgc cca gga gca ggc atc      384
Gly Glu Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile
          115                      120                      125

agc tcc ctc cag aca gtg ccc gtg acc ctc ctg ggg cct agg gcc tgc      432
Ser Ser Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys
          130                      135                      140

agc cgg ctg cat gca gct cct ggg ggt gat ggc agc cct att ctg ccg      480
Ser Arg Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro
145                      150                      155                      160

ggg atg gtg tgt acc agt gct gtg ggt gag ctg ccc agc tgt gag ggc      528
Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly
          165                      170                      175

ctg tct ggg gca cca ctg gtg cat gag gtg agg ggc aca tgg ttc ctg      576
Leu Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
          180                      185                      190

gcc ggg ctg cac agc ttc gga gat gct tgc caa ggc ccc gcc agg ccg      624
Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro
          195                      200                      205

gcg gtc ttc acc gcg ctc cct gcc tat gag gac tgg gtc agc agt ttg      672
Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu
          210                      215                      220

gac tgg cag gtc tac ttc gcc gag gaa cca gag ccc gag gct gag cct      720
Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro
225                      230                      235                      240

gga agc tgc ctg gcc aac atg agt atg tgg ccc cgg ggc ctc ctg cca      768
Gly Ser Cys Leu Ala Asn Met Ser Met Trp Pro Arg Gly Leu Leu Pro
          245                      250                      255

aac cct gcc tct cca gga ccc ttc tct ctc cag tga      804
Asn Pro Ala Ser Pro Gly Pro Phe Ser Leu Gln *
          260                      265

```

<210> 274
 <211> 267
 <212> PRT
 <213> Homo Sapien

```

<400> 274
Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp Pro Trp Glu Ala
 1          5          10          15
Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly Gly Ala Leu Val Ser
          20          25          30
Glu Glu Thr Val Leu Thr Val Ala His Cys Phe Ile Gly Arg Gln Ala
          35          40          45
Pro Glu Glu Trp Ser Val Gly Leu Gly Thr Arg Pro Glu Glu Trp Gly
          50          55          60
Leu Lys Gln Leu Ile Leu His Gly Ala Tyr Thr His Pro Glu Gly Gly
65          70          75          80

```

-169-

Tyr Asp Met Ala Leu Leu Leu Leu Ala Gln Pro Val Thr Leu Gly Ala
 85 90 95
 Ser Leu Arg Pro Leu Cys Leu Pro Tyr Pro Asp His His Leu Pro Asp
 100 105 110
 Gly Glu Arg Gly Trp Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile
 115 120 125
 Ser Ser Leu Gln Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys
 130 135 140
 Ser Arg Leu His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro
 145 150 155 160
 Gly Met Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly
 165 170 175
 Leu Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu
 180 185 190
 Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg Pro
 195 200 205
 Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser Ser Leu
 210 215 220
 Asp Trp Gln Val Tyr Phe Ala Glu Glu Pro Glu Pro Glu Ala Glu Pro
 225 230 235 240
 Gly Ser Cys Leu Ala Asn Met Ser Met Trp Pro Arg Gly Leu Leu Pro
 245 250 255
 Asn Pro Ala Ser Pro Gly Pro Phe Ser Leu Gln
 260 265

<210> 275

<211> 699

<212> DNA

<213> Homo Sapien

<220>

<221> CDS

<222> (1)...(699)

 <223> Nucleotide sequence encoding MTSP22, including
 MTSP22 protease domain

<400> 275

att gtg aat gga aaa agc tcc ctg gag ggg gca tgg cca tgg cag gcc	48
Ile Val Asn Gly Lys Ser Ser Leu Glu Gly Ala Trp Pro Trp Gln Ala	
1 5 10 15	
agc atg caa tgg aaa ggc cgt cac tac tgt gga gcc tct ctg atc agc	96
Ser Met Gln Trp Lys Gly Arg His Tyr Cys Gly Ala Ser Leu Ile Ser	
20 25 30	
agc agg tgg cta tta tct gca gct cac tgc ttt gct aag aaa aat aat	144
Ser Arg Trp Leu Leu Ser Ala Ala His Cys Phe Ala Lys Lys Asn Asn	
35 40 45	
tca aaa gat tgg act gtc aac ttt gga gtt gta gta aat aaa cca tat	192
Ser Lys Asp Trp Thr Val Asn Phe Gly Val Val Val Asn Lys Pro Tyr	
50 55 60	
atg aca cgg aaa gtc caa aac att att ttt cat gaa aat tat agc agt	240
Met Thr Arg Lys Val Gln Asn Ile Ile Phe His Glu Asn Tyr Ser Ser	
65 70 75 80	
cct ggg ctt cat gat gat att gcc ctt gtg cag ctt gct gaa gaa gtt	288
Pro Gly Leu His Asp Asp Ile Ala Leu Val Gln Leu Ala Glu Glu Val	
85 90 95	

-170-

tct ttt aca gag tac att cgt aag att tgt ctt cct gaa gcc aaa atg 336
 Ser Phe Thr Glu Tyr Ile Arg Lys Ile Cys Leu Pro Glu Ala Lys Met
 100 105 110

aag ctc tca gaa aat gac aat gtt gta gtt aca ggt tgg gga aca ctt 384
 Lys Leu Ser Glu Asn Asp Asn Val Val Val Thr Gly Trp Gly Thr Leu
 115 120 125

tat atg aat ggt tca ttt cca gtg ata ctt caa gaa gcc ttt ttg aag 432
 Tyr Met Asn Gly Ser Phe Pro Val Ile Leu Gln Glu Ala Phe Leu Lys
 130 135 140

att att gac aac aaa att tgc aat gcc tca tat gca tac tct ggc tta 480
 Ile Ile Asp Asn Lys Ile Cys Asn Ala Ser Tyr Ala Tyr Ser Gly Leu
 145 150 155 160

gtg act gat aca atg tta tgt gct gga ttt atg tca gga gaa gct gat 528
 Val Thr Asp Thr Met Leu Cys Ala Gly Phe Met Ser Gly Glu Ala Asp
 165 170 175

gca tgt cag aat gat tct ggt gga cca cta gct tac cct gat tcc aga 576
 Ala Cys Gln Asn Asp Ser Gly Gly Pro Leu Ala Tyr Pro Asp Ser Arg
 180 185 190

aat atc tgg cat ctt gtt gga ata gta agc tgg ggt gat gga tgt ggt 624
 Asn Ile Trp His Leu Val Gly Ile Val Ser Trp Gly Asp Gly Cys Gly
 195 200 205

aaa aag aat aag cca ggt gtc tat act cga gtg act tct tat cgc aat 672
 Lys Lys Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ser Tyr Arg Asn
 210 215 220

tgg att aca tcc aag act gga ctc tga 699
 Trp Ile Thr Ser Lys Thr Gly Leu *
 225 230

<210> 276
 <211> 232
 <212> PRT
 <213> Homo Sapien

<400> 276
 Ile Val Asn Gly Lys Ser Ser Leu Glu Gly Ala Trp Pro Trp Gln Ala
 1 5 10 15
 Ser Met Gln Trp Lys Gly Arg His Tyr Cys Gly Ala Ser Leu Ile Ser
 20 25 30
 Ser Arg Trp Leu Leu Ser Ala Ala His Cys Phe Ala Lys Lys Asn Asn
 35 40 45
 Ser Lys Asp Trp Thr Val Asn Phe Gly Val Val Val Asn Lys Pro Tyr
 50 55 60
 Met Thr Arg Lys Val Gln Asn Ile Ile Phe His Glu Asn Tyr Ser Ser
 65 70 75 80
 Pro Gly Leu His Asp Asp Ile Ala Leu Val Gln Leu Ala Glu Glu Val
 85 90 95
 Ser Phe Thr Glu Tyr Ile Arg Lys Ile Cys Leu Pro Glu Ala Lys Met
 100 105 110
 Lys Leu Ser Glu Asn Asp Asn Val Val Val Thr Gly Trp Gly Thr Leu
 115 120 125
 Tyr Met Asn Gly Ser Phe Pro Val Ile Leu Gln Glu Ala Phe Leu Lys
 130 135 140

-171-

Ile	Ile	Asp	Asn	Lys	Ile	Cys	Asn	Ala	Ser	Tyr	Ala	Tyr	Ser	Gly	Leu
145					150					155					160
Val	Thr	Asp	Thr	Met	Leu	Cys	Ala	Gly	Phe	Met	Ser	Gly	Glu	Ala	Asp
				165					170						175
Ala	Cys	Gln	Asn	Asp	Ser	Gly	Gly	Pro	Leu	Ala	Tyr	Pro	Asp	Ser	Arg
			180					185					190		
Asn	Ile	Trp	His	Leu	Val	Gly	Ile	Val	Ser	Trp	Gly	Asp	Gly	Cys	Gly
		195					200					205			
Lys	Lys	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Thr	Ser	Tyr	Arg	Asn
	210					215					220				
Trp	Ile	Thr	Ser	Lys	Thr	Gly	Leu								

<210> 277
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> ACETYLATION
 <222> 1

<221> MOD_RES
 <222> 6
 <223> Leucine-therapeutic agent

<223> conjugate

<400> 277
 Gly Ser Gly Arg Ser Xaa
 1 5

<210> 278
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> ACETYLATION
 <222> 1

<221> MOD_RES
 <222> 6
 <223> Xaa is Leucine-therapeutic Agent

<223> conjugate

<400> 278
 Gly Ser Gly Arg Ser Xaa
 1 5

<210> 279
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> ACETYLATION
 <222> 1

-172-

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 279
Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 280
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 280
Gly Ser Gly Arg Xaa
1 5

<210> 281
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> AMIDATION
<222> 6

<221> MOD_RES
<222> 4
<223> Xaa is 4-Guanidino-phenylglycine

<223> conjugate

<400> 281
Gly Ser Gly Xaa Ser Leu
1 5

<210> 282
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION

-173-

<222> 1

<221> MOD_RES

<222> 7

<223> Cyclohexylamine-therapeutic Agent

<223> conjugate

<400> 282

Gly Ser Gly Arg Ser Ser Xaa

1

5

<210> 283

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic agent

<223> conjugate

<400> 283

Gly Ser Gly Arg Ala Ser Xaa

1

5

<210> 284

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Nle-therapeutic agent

<223> conjugate

<400> 284

Gly Ser Gly Arg Ser Xaa

1

5

<210> 285

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> (0)...(0)

-174-

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 285
Gly Thr Gly Arg Ser Xaa
1 5

<210> 286
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Succinyl-BAlanine

<221> MOD_RES
<222> 6
<223> Nle-therapeutic Agent

<223> conjugate

<400> 286
Ala Thr Gly Arg Ser Xaa
1 5

<210> 287
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 287
Gly Thr Gly Arg Ser Xaa
1 5

<210> 288
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

-175-

<221> MOD_RES
<222> 2
<223> Xaa is Homoserine

<221> MOD_RES
<222> 6
<223> Nle-Therapeutic AgentNle

<223> conjugate

<400> 288
Gly Xaa Gly Arg Ser Xaa
1 5

<210> 289
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is D Serine

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 289
Gly Xaa Ala Arg Ser Xaa
1 5

<210> 290
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 290
Gly Ser Ala Arg Ser Xaa
1 5

<210> 291
<211> 7

-176-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 291
Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 292
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 292
Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 293
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 293
Gly Ser Ala Arg Ala Ser Xaa
1 5

<210> 294
<211> 6
<212> PRT

-177-

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 294

Val Ser Gly Arg Ser Xaa
1 5

<210> 295

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 295

Val Ser Gly Arg Ala Xaa
1 5

<210> 296

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 296

Val Ser Gly Arg Ala Ser Xaa
1 5

<210> 297

<211> 7

<212> PRT

<213> Artificial Sequence

-178-

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 297
Val Ser Gly Arg Ser Ser Xaa
1 5

<210> 298
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 298
Val Ser Ala Arg Met Xaa
1 5

<210> 299
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Xaa is Nle

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 299
Val Ser Ala Arg Xaa Xaa
1 5

<210> 300
<211> 6

-179-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 300
Val Ser Ala Arg Ser Xaa
1 5

<210> 301
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 301
Val Ser Ala Arg Ser Xaa
1 5

<210> 302
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> dValine-therapeutic Agent

<223> conjugate

<400> 302
Xaa Pro Gly Arg Val Xaa
1 5

-180-

<210> 303
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Valine-therapeutic Agent

<223> conjugate

<400> 303
Xaa Pro Gly Arg Val Xaa
1 5

<210> 304
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 304
Xaa Pro Gly Arg Ala Xaa
1 5

<210> 305
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

-181-

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 305
Xaa Pro Gly Arg Ser Xaa
1 5

<210> 306
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 306
Xaa Pro Ala Arg Ser Xaa
1 5

<210> 307
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 307
Xaa Pro Ala Arg Ala Ser Xaa
1 5

<210> 308
<211> 6

-182-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is t-Butyl Glycine

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 308
Xaa Pro Gly Arg Ser Xaa
1 5

<210> 309
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is D Serine

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 309
Arg Gly Xaa Ala Arg Ser Xaa
1 5

<210> 310
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

-183-

<400> 310
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 311
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 311
Arg Gly Ser Gly Ala Xaa
1 5

<210> 312
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 312
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 313
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<223> conjugate

<400> 313

-184-

Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 314
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<223> conjugate

<400> 314
Arg Gly Ser Gly Arg Ala Xaa
1 5

<210> 315
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 315
Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 316
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 316
Arg Gly Ser Gly Arg Ser Xaa

-185-

1

5

<210> 317
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 317
Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 318
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 318
Arg Gly Ser Ala Arg Ser Xaa
1 5

<210> 319
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 319
Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

-186-

<210> 320
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nva-therapeutic agent

<223> conjugate

<400> 320
Arg Gly Ser Ala Arg Ser Xaa
1 5

<210> 321
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Nva-therapeutic agent

<223> conjugate

<400> 321
Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 322
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 322
Arg Gly Ser Ala Arg Ser Xaa
1 5

-187-

<210> 323
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is S-MethylCysteine

<221> MOD_RES
<222> 7
<223> Valine-therapeutic Agent

<223> conjugate

<400> 323
Arg Xaa Pro Gly Arg Val Xaa
1 5

<210> 324
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 7
<223> Valine-therapeutic Agent

<223> conjugate

<400> 324
Arg Xaa Pro Gly Arg Val Xaa
1 5

<210> 325
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is S-Methylcysteine

-188-

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 325
Arg Xaa Pro Gly Arg Ser Xaa
1 5

<210> 326
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 326
Arg Leu Pro Gly Arg Ser Xaa
1 5

<210> 327
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> VARIANT
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 327
Arg Val Pro Gly Arg Ser Xaa
1 5

<210> 328
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> VARIANT

-189-

<222> 8
<223> dLeucine-therapeutic Agent

<223> conjugate

<400> 328
Arg Val Pro Gly Arg Ser Xaa
1 5

<210> 329
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Nle

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 329
Arg Xaa Pro Gly Arg Ser Xaa
1 5

<210> 330
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is t-Butylglycine

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 330
Arg Xaa Pro Ala Arg Ser Xaa
1 5

<210> 331
<211> 7
<212> PRT

-190-

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 331

Arg Leu Pro Ala Arg Ser Xaa
1 5

<210> 332

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 332

Arg Val Pro Ala Arg Ser Xaa
1 5

<210> 333

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 2

<223> Xaa is Nle

<221> MOD_RES

<222> 7

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 333

Arg Xaa Pro Ala Arg Ser Xaa
1 5

-191-

<210> 334
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 334
Ile Val Ser Gly Arg Ala Xaa
1 5

<210> 335
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 335
Ile Val Ser Gly Arg Ser Ser Xaa
1 5

<210> 336
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 336
Ile Val Ser Gly Arg Ala Ser Xaa
1 5

<210> 337

-192-

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 337
Ile Val Ser Ala Arg Met Xaa
1 5

<210> 338
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Xaa is Nle

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 338
Ile Val Ser Ala Arg Xaa Xaa
1 5

<210> 339
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 339
Ile Val Ser Ala Arg Ser Xaa
1 5

-193-

<210> 340
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic Agent

<223> conjugate

<400> 340
Ile Val Ser Ala Arg Ser Xaa
1 5

<210> 341
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 341
Ile Val Ser Ala Arg Ser Ser Xaa
1 5

<210> 342
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> VARIANT
<222> 8
<223> dLeucine-therapeutic Agent

<223> conjugate

<400> 342
Leu Arg Gly Ser Gly Arg Ser Xaa
1 5

-194-

<210> 343
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 343
Leu Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 344
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Nle-therapeutic agent

<223> conjugate

<400> 344
Leu Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 345
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 345
Leu Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 346

-195-

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 346
Leu Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 347
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 347
Leu Arg Gly Ser Ala Arg Ser Xaa
1 5

<210> 348
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 348
Leu Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 349
<211> 9

-196-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Nva-therapeutic agent

<223> conjugate

<400> 349
Leu Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 350
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Nle-therapeutic agent

<223> conjugate

<400> 350
Leu Arg Gly Ser Ala Arg Ser Ser Xaa
1 5

<210> 351
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 351
Val Ile Val Ser Gly Arg Ala Xaa
1 5

<210> 352
<211> 8
<212> PRT

-197-

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 352

Val Ile Val Ser Ala Arg Ser Xaa
1 5

<210> 353

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 353

Val Ile Val Ser Gly Arg Ser Ser Xaa
1 5

<210> 354

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic Agent

<223> conjugate

<400> 354

Val Ile Val Ser Ala Arg Met Xaa
1 5

<210> 355

<211> 8

<212> PRT

<213> Artificial Sequence

-198-

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Xaa is Nle

<221> MOD_RES
<222> 8
<223> Alanine-therapeutic Agent

<223> conjugate

<400> 355
Val Ile Val Ser Ala Arg Xaa Xaa
1 5

<210> 356
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Nle-therapeutic agent

<223> conjugate

<400> 356
Val Ile Val Ser Ala Arg Ser Xaa
1 5

<210> 357
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> dCyclohexylalanine-therapeutic agent

<223> conjugate

<400> 357
Val Ile Val Ser Ala Arg Ser Xaa
1 5

<210> 358
<211> 8

-199-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 358
Val Ile Val Ser Ala Arg Ser Xaa
1 5

<210> 359
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 9
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 359
Val Ile Val Ser Ala Arg Ser Ser Xaa
1 5

<210> 360
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is S-methylcysteine

<221> MOD_RES
<222> 9
<223> Valine-therapeutic Agent

<223> conjugate

<400> 360
Arg Arg Xaa Pro Gly Arg Val Xaa
1 5

-200-

<210> 361
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is Nva

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 361
Arg Arg Xaa Pro Ala Arg Ser Xaa
1 5

<210> 362
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 362
Ser Gly Arg Ser Xaa
1 5

<210> 363
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 363
Ser Gly Arg Ser Ser Xaa

-201-

1

5

<210> 364
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 364
Ser Gly Arg Ser Ser Ser Xaa
1 5

<210> 365
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 365
Ser Gly Arg Ser Xaa
1 5

<210> 366
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> dNva-therapeutic agent

<223> conjugate

<400> 366
Ser Gly Arg Ser Xaa
1 5

-202-

<210> 367
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nva-therapeutic agent

<223> conjugate

<400> 367
Ser Gly Arg Ser Xaa
1 5

<210> 368
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 5
<223> Hexylglycine-therapeutic agent

<223> conjugate

<400> 368
Ser Gly Arg Ser Xaa
1 5

<210> 369
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 369
Ser Gly Arg Ser Xaa
1 5

-203-

<210> 370
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Homocyclohexylalanine-therapeutic agent

<223> conjugate

<400> 370
Ser Gly Arg Ser Xaa
1 5

<210> 371
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 371
Ser Ala Arg Ser Ser Xaa
1 5

<210> 372
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 372
Ser Ala Arg Ser Ser Xaa
1 5

<210> 373

-204-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 373
Ser Ser Arg Ser Xaa
1 5

<210> 374
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Abu-therapeutic agent

<223> conjugate

<400> 374
Thr Gly Arg Ser Xaa
1 5

<210> 375
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 375
Thr Gly Arg Ser Xaa
1 5

<210> 376
<211> 5

-205-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nva-therapeutic agent

<223> conjugate

<400> 376
Thr Gly Arg Ser Xaa
1 5

<210> 377
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 377
Thr Gly Arg Ser Xaa
1 5

<210> 378
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Hexylglycine-therapeutic agent

<223> conjugate

<400> 378
Thr Gly Arg Ser Xaa
1 5

<210> 379
<211> 5
<212> PRT

-206-

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 379

Thr Gly Arg Ser Xaa
1 5

<210> 380

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Homocyclohexylalanine-therapeutic agent

<223> conjugate

<400> 380

Thr Gly Arg Ser Xaa
1 5

<210> 381

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Abu-therapeutic agent

<223> conjugate

<400> 381

Thr Gly Arg Thr Xaa
1 5

<210> 382

<211> 5

<212> PRT

<213> Artificial Sequence

-207-

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Homoserine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 382
Thr Gly Arg Xaa Xaa
1 5

<210> 383
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Abu

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 383
Thr Gly Arg Xaa Xaa
1 5

<210> 384
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 4
<223> Xaa is Abu

<221> MOD_RES
<222> 5
<223> Nva-therapeutic agent

<223> conjugate

-208-

<400> 384
Thr Gly Arg Xaa Xaa
1 5

<210> 385
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is 4-Guanidinophenylalanine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 385
Thr Gly Xaa Ser Xaa
1 5

<210> 386
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is 4-Guanidinophenylalanine

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 386
Thr Gly Xaa Ser Xaa
1 5

<210> 387
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

-209-

<221> MOD_RES
<222> 3
<223> Xaa is 4-Guanidinophenylalanine

<221> MOD_RES
<222> 4
<223> Xaa is Abu

<221> MOD_RES
<222> 5
<223> Nva-therapeutic agent

<223> conjugate

<400> 387
Thr Gly Xaa Xaa Xaa
1 5

<210> 388
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is Alloc

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 388
Thr Gly Xaa Ser Xaa
1 5

<210> 389
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 389
Thr Gly Lys Ser Xaa
1 5

-210-

<210> 390
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is Homoarginine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 390
Thr Gly Xaa Ser Xaa
1 5

<210> 391
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is N-homoserine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 391
Xaa Gly Arg Ser Xaa
1 5

<210> 392
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is N-Methyloxycarbonyl threonine

<221> MOD_RES
<222> 5

-211-

<223> Nle-therapeutic agent

<223> conjugate

<400> 392

Xaa Gly Arg Ser Xaa
1 5

<210> 393

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Phenylsulfonyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 393

Xaa Gly Arg Ser Xaa
1 5

<210> 394

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Methoxyethylcarbonyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 394

Xaa Gly Arg Ser Xaa
1 5

<210> 395

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Methoxydiethoxyacetyl threonine

-212-

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 395
Xaa Gly Arg Ser Xaa
1 5

<210> 396
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is 4-Oxo-pentanoyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 396
Xaa Gly Arg Ser Xaa
1 5

<210> 397
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is 2-Benzo[1,3]dioxol-5-yl acetylthreonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 397
Xaa Gly Arg Ser Xaa
1 5

<210> 398
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1

-213-

<223> Xaa is 2-Pyridin-2-yl-acetyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 398

Xaa Gly Arg Ser Xaa
1 5

<210> 399

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Benzoylacetyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 399

Xaa Gly Arg Ser Xaa
1 5

<210> 400

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is 2-Hydroxy-3-phenyl propionylacetyl
threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 400

Thr Gly Arg Ser Xaa
1 5

<210> 401

<211> 5

<212> PRT

<213> Artificial Sequence

-214-

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Methoxyacetylthreonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 401
Xaa Gly Arg Ser Xaa
1 5

<210> 402
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Phenylacetyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 402
Xaa Gly Arg Ser Xaa
1 5

<210> 403
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is 3-Methoxypropionyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 403
Thr Gly Arg Ser Xaa
1 5

<210> 404
<211> 5
<212> PRT

-215-

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Methoxyethoxyacetyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 404

Thr Gly Arg Ser Xaa
1 5

<210> 405

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is 1-Carboxybutanoyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 405

Thr Gly Arg Ser Xaa
1 5

<210> 406

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> MOD_RES

<222> 1

<223> Xaa is Carboxybenzyl threonine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 406

Xaa Gly Arg Ser Xaa
1 5

<210> 407

-216-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Ethoxycarbonylthreonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 407
Xaa Gly Arg Ser Xaa
1 5

<210> 408
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is BALanine

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 408
Xaa Thr Gly Arg Ser Xaa
1 5

<210> 409
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Pent-4-ynoyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 409
Xaa Gly Arg Ser Xaa
1 5

-217-

<210> 410
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Naphthaacetyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 410
Xaa Gly Arg Ser Xaa
1 5

<210> 411
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Isobutyloxycarbonyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 411
Xaa Gly Arg Ser Xaa
1 5

<210> 412
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Hydroxyacetyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 412
Xaa Gly Arg Ser Xaa
1 5

-218-

<210> 413
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarboxylpropanoyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 413
Xaa Gly Arg Ser Xaa
1 5

<210> 414
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is N,N-dimethyl glycine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 414
Xaa Gly Arg Ser Xaa
1 5

<210> 415
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Succinyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 415
Xaa Gly Arg Ser Xaa

-219-

1

5

<210> 416
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> 1
<223> Xaa is Formyl threonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 416
Xaa Gly Arg Ser Xaa
1 5

<210> 417
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 417
Thr Ala Arg Ser Xaa
1 5

<210> 418
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is 4-Guanidinophenylalanine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

-220-

<223> conjugate

<400> 418

Thr Ala Xaa Ser Xaa
1 5

<210> 419

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is Abu

<221> MOD_RES

<222> 5

<223> Nva-therapeutic agent

<223> conjugate

<400> 419

Thr Ala Arg Xaa Xaa
1 5

<210> 420

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Abu-therapeutic agent

<223> conjugate

<400> 420

Thr Ala Arg Ser Xaa
1 5

<210> 421

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

-221-

<222> 5
<223> Abu-therapeutic agent

<223> conjugate

<400> 421
Thr Ala Arg Thr Xaa
1 5

<210> 422
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Serine methyl ester

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 422
Thr Xaa Arg Ser Xaa
1 5

<210> 423
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Homoserine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 423
Thr Xaa Arg Ser Xaa
1 5

<210> 424
<211> 5
<212> PRT

-222-

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 2

<223> Xaa is 1-Methyl histidine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 424

Thr Xaa Arg Ser Xaa
1 5

<210> 425

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 2

<223> Xaa is 3-Methyl histidine

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 425

Thr Xaa Arg Ser Xaa
1 5

<210> 426

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 5

<223> Nle-therapeutic agent

<223> conjugate

<400> 426

-223-

Thr His Arg Ser Xaa
1 5

<210> 427
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is MeGlycine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 427
Thr Xaa Arg Ser Xaa
1 5

<210> 428
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Nva

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 428
Thr Xaa Arg Ser Xaa
1 5

<210> 429
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

-224-

<221> MOD_RES
<222> 2
<223> Xaa is Nle

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 429
Thr Xaa Arg Ser Xaa
1 5

<210> 430
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 5
<223> Cyclohexyl alanine-therapeutic agent

<223> conjugate

<400> 430
Thr Ala Arg Ser Xaa
1 5

<210> 431
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Abu

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 431
Thr Xaa Arg Ser Xaa
1 5

<210> 432
<211> 5

-225-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is 4,4-Dimethylthreonine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 432
Xaa Gly Arg Ser Xaa
1 5

<210> 433
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is Homoserine

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 433
Xaa Gly Arg Ser Xaa
1 5

<210> 434
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1,4
<223> Xaa is Homoserine

<221> MOD_RES
<222> 5

-226-

<223> Cyclohexyl alanine-therapeutic agent

<223> conjugate

<400> 434

Xaa Gly Arg Xaa Xaa
1 5

<210> 435

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is Homoserine

<221> MOD_RES

<222> 5

<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 435

Xaa Gly Arg Ser Xaa
1 5

<210> 436

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is Homoserine

<221> MOD_RES

<222> 5

<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 436

Xaa Gly Arg Thr Xaa
1 5

<210> 437

<211> 5

<212> PRT

<213> Artificial Sequence

-227-

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is Homoserine

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 437
Xaa Ala Arg Ser Xaa
1 5

<210> 438
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Nle-therapeutic agent

<223> conjugate

<400> 438
Asn Gly Arg Ser Xaa
1 5

<210> 439
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 439
Tyr Gly Arg Ser Ser Xaa
1 5

<210> 440
<211> 5

-228-

<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 440
Tyr Gly Arg Ser Xaa
1 5

<210> 441
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<223> conjugate

<400> 441
Gln Gly Arg Ser Ser Xaa
1 5

<210> 442
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<223> conjugate

<400> 442
Gln Gly Arg Ser Ser Xaa
1 5

<210> 443
<211> 4
<212> PRT

-229-

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is N-homoserine

<221> MOD_RES

<222> 4

<223> Nle-therapeutic agent

<223> conjugate

<400> 443

Xaa Arg Ser Xaa

1

<210> 444

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is N-homoserine

<221> MOD_RES

<222> 4

<223> Nva-therapeutic agent

<223> conjugate

<400> 444

Xaa Arg Ser Xaa

1

<210> 445

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> ACETYLATION

<222> 1

<221> BLOCKED

<222> 5

<223> Leucine-therapeutic Agent

<223> conjugate

<400> 445

-230-

Gln Gly Arg Ser Xaa
1 5

<210> 446
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 446
Gln Gly Arg Ser Ser Xaa
1 5

<210> 447
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 447
Gln Gly Arg Ala Ser Xaa
1 5

<210> 448
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic Agent

<223> conjugate

<400> 448
Asn Gly Arg Ser Ser Xaa

-231-

1

5

<210> 449
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nleucine-therapeutic agent

<223> conjugate

<400> 449
Gln Gly Arg Ser Ser Xaa
1 5

<210> 450
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nvaline-therapeutic agent

<223> conjugate

<400> 450
Gln Gly Arg Ser Ser Xaa
1 5

<210> 451
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<223> conjugate

<400> 451
Gln Gly Arg Ser Ser Xaa
1 5

-232-

<210> 452
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Allyl-therapeutic agent

<223> conjugate

<221> MOD_RES
<222> 5
<223> Xaa is dSerine

<400> 452
Gln Gly Arg Ser Xaa Xaa
1 5

<210> 453
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Allyl-therapeutic agent

<400> 453
Gln Gly Arg Ser Ser Xaa
1 5

<210> 454
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 454

-233-

Gln Ala Arg Ser Xaa
1 5

<210> 455
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 455
Gln Ala Arg Ser Ser Xaa
1 5

<210> 456
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 456
Gln Ser Arg Ser Xaa
1 5

<210> 457
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 457
Gln Ser Arg Ser Ser Xaa

-234-

1

5

<210> 458
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 458
Gln Ser Arg Ser Ser Xaa
1 5

<210> 459
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 459
Gln Ser Arg Ser Ser Xaa
1 5

<210> 460
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 460
Gln Thr Arg Ser Ser Xaa
1 5

-235-

<210> 461
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Aib

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 461
Gln Xaa Arg Ser Ser Xaa
1 5

<210> 462
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Aib

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 462
Gln Xaa Arg Ser Ser Xaa
1 5

<210> 463
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES

-236-

<222> 2
<223> Xaa is Abu

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 463
Gln Xaa Arg Ser Ser Xaa
1 5

<210> 464
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Abu

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 464
Gln Xaa Arg Ser Ser Xaa
1 5

<210> 465
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2
<223> Xaa is Cyclohexylalanine

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 465
Gln Xaa Arg Ser Ser Xaa
1 5

<210> 466

-237-

<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 466
Gln Phe Arg Ser Xaa
1 5

<210> 467
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 467
Gln Phe Arg Ser Ser Xaa
1 5

<210> 468
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 468
Gln Tyr Arg Ser Ser Xaa
1 5

<210> 469
<211> 5

-238-

<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 469
Arg Gly Arg Ser Xaa
1 5

<210> 470
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 470
Arg Gly Arg Ser Ser Xaa
1 5

<210> 471
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 471
Arg Gly Arg Ser Ser Xaa
1 5

<210> 472
<211> 5
<212> PRT

-239-

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Cyclohexylalanine-therapeutic agent

<400> 472

Arg Gly Arg Ser Xaa
1 5

<210> 473

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 473

Arg Ala Arg Ser Xaa
1 5

<210> 474

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 474

Arg Ala Arg Ser Ser Xaa
1 5

<210> 475

<211> 5

<212> PRT

<213> Artificial Sequence

-240-

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 475
Arg Ser Arg Ser Xaa
1 5

<210> 476
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 476
Arg Ser Arg Ser Ser Xaa
1 5

<210> 477
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<400> 477
Arg Ser Arg Ser Xaa
1 5

<210> 478
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

-241-

<223> conjugate
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 478
Arg Ser Arg Ser Ser Xaa
1 5

<210> 479
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 479
Arg Phe Arg Ser Xaa
1 5

<210> 480
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Cyclohexylalanine-therapeutic agent

<400> 480
Arg Phe Arg Ser Xaa
1 5

<210> 481
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

-242-

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 481

Tyr Gly Arg Ser Ser Xaa
1 5

<210> 482

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is S-Dioxomethionine

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 482

Xaa Ser Arg Ser Xaa
1 5

<210> 483

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-(alpha-(3-cyanobenzyl))
glutamic acid-delta-methyl ester

<221> AMIDATION

<222> 5

<400> 483

Xaa Gly Arg Ser Leu
1 5

<210> 484

<211> 5

<212> PRT

<213> Artificial Sequence

-243-

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-amidinobenzyl))
glutamic acid -delta-methyl ester

<221> AMIDATION
<222> 5

<400> 484
Xaa Gly Arg Ser Leu
1 5

<210> 485
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-
(alpha-(3-amidinobenzyl)) glutamic acid

<221> AMIDATION
<222> 5

<400> 485
Xaa Gly Arg Ser Leu
1 5

<210> 486
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-Methylbenzyl)
)glutamic acid -delta-methyl ester

<221> AMIDATION
<222> 5

<400> 486
Xaa Gly Arg Ser Leu
1 5

<210> 487
<211> 5
<212> PRT

-244-

<213> Artificial Sequence

<220>

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-
(alpha-(3-methylbenzyl)) glutamic acid

<221> AMIDATION

<222> 5

<400> 487

Xaa Gly Arg Ser Leu
1 5

<210> 488

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-(alpha-(3-cyanobenzyl))
glutamic acid-delta-methyl ester

<221> AMIDATION

<222> 6

<400> 488

Xaa Gly Arg Ser Ser Leu
1 5

<210> 489

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-(alpha-(3-methylbenzyl)
)glutamic acid -delta-methyl ester

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 489

Xaa Gly Arg Ser Xaa
1 5

-245-

<210> 490
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-cyanobenzyl))
glutamic acid -delta-methyl ester

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 490
Xaa Gly Arg Ser Xaa
1 5

<210> 491
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 491
Arg Gln Gly Arg Ser Xaa
1 5

<210> 492
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 492
Arg Gln Gly Arg Ser Ser Xaa
1 5

-246-

<210> 493
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 493
Arg Gln Gly Arg Ser Xaa
1 5

<210> 494
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 494
Arg Gln Gly Arg Ser Xaa
1 5

<210> 495
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Phenylalanine-therapeutic agent

<400> 495
Arg Gln Gly Arg Ser Xaa
1 5

<210> 496

-247-

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> dLeucine-therapeutic agent

<400> 496
Arg Gln Gly Arg Ala Xaa
1 5

<210> 497
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 497
Arg Gln Gly Arg Ala Xaa
1 5

<210> 498
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> dNle-therapeutic agent

<400> 498
Arg Gln Gly Arg Ala Xaa
1 5

<210> 499
<211> 6

-248-

<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 499
Arg Gln Gly Arg Ala Xaa
1 5

<210> 500
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 500
Arg Gln Gly Arg Ala Xaa
1 5

<210> 501
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 501
Arg Gln Gly Arg Ala Xaa
1 5

<210> 502
<211> 6
<212> PRT

-249-

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Phenylalanine-therapeutic agent

<400> 502

Arg Gln Gly Arg Ala Xaa
1 5

<210> 503

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> leucine-therapeutic agent

<400> 503

Arg Asn Gly Arg Ser Xaa
1 5

<210> 504

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Nle-therapeutic agent

<400> 504

Arg Asn Gly Arg Ala Xaa
1 5

<210> 505

<211> 6

<212> PRT

<213> Artificial Sequence

-250-

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 505
Arg Gln Ala Arg Ser Xaa
1 5

<210> 506
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 506
Arg Gln Ala Arg Ser Xaa
1 5

<210> 507
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 507
Arg Gln Ala Arg Ser Xaa
1 5

<210> 508
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

-251-

<223> conjugate
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 508
Arg Gln Ala Arg Ser Xaa
1 5

<210> 509
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Cyclohexylalanine-therapeutic agent

<400> 509
Arg Gln Ala Arg Ser Ser Xaa
1 5

<210> 510
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 510
Arg Gln Ala Arg Thr Xaa
1 5

<210> 511
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

-252-

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 511
Arg Gln Ala Arg Ala Xaa
1 5

<210> 512
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 512
Arg Gln Ala Arg Ala Xaa
1 5

<210> 513
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 513
Arg Gln Ala Arg Ala Xaa
1 5

<210> 514
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION

-253-

<222> 1

<221> MOD_RES

<222> 6

<223> Cyclohexylalanine-therapeutic agent

<400> 514

Arg Gln Ala Arg Ala Xaa
1 5

<210> 515

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 515

Arg Gln Ser Arg Ala Xaa
1 5

<210> 516

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 516

Arg Gln Ser Arg Xaa
1 5

<210> 617

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

-254-

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 517
Arg Gln Ser Arg Ala Xaa
1 5

<210> 518
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 518
Arg Gln Ser Arg Ala Xaa
1 5

<210> 519
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 519
Arg Gln Ser Arg Ala Xaa
1 5

<210> 520
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES

-255-

<222> 6
<223> Nva-therapeutic agent

<400> 520
Arg Gln Ser Arg Ala Xaa
1 5

<210> 521
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 521
Arg Gln Ser Arg Ala Xaa
1 5

<210> 522
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 522
Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 523
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6

-256-

<223> Leucine-therapeutic agent

<400> 523

Arg Gln Ser Arg Ser Xaa
1 5

<210> 524

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> dNle-therapeutic agent

<400> 524

Arg Gln Ser Arg Ser Xaa
1 5

<210> 525

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Nle-therapeutic agent

<400> 525

Arg Gln Ser Arg Ser Xaa
1 5

<210> 526

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Nva-therapeutic agent

-257-

<400> 526
Arg Gln Ser Arg Ser Xaa
1 5

<210> 527
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Allylglycine-therapeutic agent

<400> 527
Arg Gln Ser Arg Ser Xaa
1 5

<210> 528
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 528
Arg Gln Ser Arg Ser Xaa
1 5

<210> 529
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle

<400> 529

-258-

Arg Gln Ser Arg Thr Xaa
1 5

<210> 530
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 530
Arg Gln Thr Arg Ser Ser Xaa
1 5

<210> 531
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 531
Arg Gln Thr Arg Ser Xaa
1 5

<210> 532
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 532
Arg Asn Ser Arg Ser Xaa

-259-

1 5

<210> 533
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 533
Arg Gln Phe Arg Ser Xaa
1 5

<210> 534
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> dNle-therapeutic agent

<400> 534
Arg Gln Phe Arg Ser Xaa
1 5

<210> 535
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 535
Arg Gln Phe Arg Ser Xaa
1 5

-260-

<210> 536
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 536
Arg Gln Phe Arg Ser Xaa
1 5

<210> 537
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 537
Arg Gln Phe Arg Ser Xaa
1 5

<210> 538
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 538
Arg Gln Phe Arg Ala Xaa
1 5

-261-

<210> 539
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 539
Arg Gln Phe Arg Ala Xaa
1 5

<210> 540
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nva-therapeutic agent

<400> 540
Arg Gln Phe Arg Ala Xaa
1 5

<210> 541
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Cyclohexylalanine-therapeutic agent

<400> 541
Arg Gln Phe Arg Ala Xaa
1 5

<210> 542

-262-

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Nle-therapeutic agent

<400> 542
Gln Ser Arg Ser Ser Xaa
1 5

<210> 543
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 543
Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 544
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 544
Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 545
<211> 7

-263-

<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 545
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 546
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<400> 546
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 547
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Nle-therapeutic agent

<400> 547
Arg Gly Ser Gly Arg Ala Xaa
1 5

<210> 548
<211> 8
<212> PRT

-264-

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 548

Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 549

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> (0)...(0)

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 549

Ile Val Ser Gly Arg Ala Ser Xaa
1 5

<210> 550

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 9

<223> Isoleucine-therapeutic agent

<400> 550

Leu Arg Arg Gln Ser Arg Ser Ser Xaa
1 5

<210> 551

<211> 8

<212> PRT

<213> Artificial Sequence

-265-

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 551
Leu Arg Arg Gln Ser Arg Ser Xaa
1 5

<210> 552
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 552
Gln Ser Arg Ala Xaa
1 5

<210> 553
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 553
Gln Ser Arg Ser Xaa
1 5

<210> 554
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

-266-

<223> conjugate
<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Glycine-therapeutic agent

<400> 554
Gln Ser Arg Ser Xaa
1 5

<210> 555
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Alanine-therapeutic agent

<400> 555
Arg Ser Arg Ala Xaa
1 5

<210> 556
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 556
Arg Gln Ser Arg Ala Xaa
1 5

<210> 557
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

-267-

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Alalnine-therapeutic agent

<400> 557
Arg Gln Ser Arg Ser Xaa
1 5

<210> 558
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 558
Arg Gln Ser Arg Ser Ala Xaa
1 5

<210> 559
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 559
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 560
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION

-268-

<222> 1

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 560

Ser Gly Arg Ala Xaa

1

5

<210> 561

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 5

<223> Alanine-therapeutic agent

<400> 561

Ser Gly Arg Ser Xaa

1

5

<210> 562

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 562

Ser Gly Arg Ser Ser Xaa

1

5

<210> 563

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

-269-

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 563
Ser Gly Arg Ala Ser Xaa
1 5

<210> 564
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Glycine-therapeutic agent

<400> 564
Ser Gly Arg Ser Xaa
1 5

<210> 565
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Glycine-therapeutic agent

<400> 565
Ser Gly Arg Ser Ser Xaa
1 5

<210> 566
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES

-270-

<222> 6
<223> Alanine-therapeutic agent

<400> 566
Ser Gly Arg Ser Gly Xaa
1 5

<210> 567
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Glycine-therapeutic agent

<400> 567
Ser Gly Arg Ser Gly Xaa
1 5

<210> 568
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Glycine-therapeutic agent

<400> 568
Gly Thr Gly Arg Ser Gly Xaa
1 5

<210> 569
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 2

-271-

<223> Xaa is D- Serine

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 569

Gly Xaa Ala Arg Ser Xaa
1 5

<210> 570

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 3

<223> Xaa is D-Serine

<221> MOD_RES

<222> 7

<223> Alanine-therapeutic agent

<400> 570

Arg Gly Xaa Ala Arg Ser Xaa
1 5

<210> 571

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Alanine-therapeutic agent

<400> 571

Gly Ser Gly Arg Ser Xaa
1 5

<210> 572

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

-272-

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 7

<223> Alanine-therapeutic agent

<400> 572

Arg Gly Ser Gly Arg Ser Xaa

1

5

<210> 573

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 573

Leu Arg Gly Ser Gly Arg Ser Xaa

1

5

<210> 574

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 4

<223> Xaa is D-Serine

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 574

Leu Arg Gly Xaa Ala Arg Ser Xaa

1

5

<210> 575

<211> 6

<212> PRT

-273-

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is S-Methylcysteine

<221> MOD_RES

<222> 6

<223> Valine-therapeutic agent

<400> 575

Xaa Pro Gly Arg Val Xaa
1 5

<210> 576

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is S-Methylcysteine

<221> MOD_RES

<222> 6

<223> Valine-therapeutic agent

<400> 576

Xaa Pro Gly Arg Val Xaa
1 5

<210> 577

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 2

<223> Xaa is S-Methylcysteine

<221> MOD_RES

-274-

<222> 7
<223> Valine-therapeutic agent

<400> 577
Arg Xaa Pro Gly Arg Val Xaa
1 5

<210> 578
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 3
<223> Xaa is S-Methylcysteine

<221> MOD_RES
<222> 8
<223> Valine-therapeutic agent

<400> 578
Arg Arg Xaa Pro Gly Arg Val Xaa
1 5

<210> 579
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 579
Val Ser Ala Arg Met Xaa
1 5

<210> 580
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION

-275-

<222> 1

<221> MOD_RES

<222> 7

<223> Alanine-therapeutic agent

<400> 580

Ile Val Ser Ala Arg Met Xaa
1 5

<210> 581

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 581

Val Ile Val Ser Ala Arg Met Xaa
1 5

<210> 582

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 7

<223> Xaa is Nle

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 582

Val Ile Val Ser Ala Arg Xaa Xaa
1 5

<210> 583

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

-276-

<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Xaa is Nle

<221> MOD_RES
<222> 6
<223> Alanine-therapeutic agent

<400> 583
Val Ser Ala Arg Xaa Xaa
1 5

<210> 584
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Xaa is Nle

<221> MOD_RES
<222> 7
<223> Alanine-therapeutic agent

<400> 584
Ile Val Ser Ala Arg Xaa Xaa
1 5

<210> 585
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 585
Gly Ser Gly Arg Ser Xaa
1 5

-277-

<210> 586
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 586
Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 587
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 587
Gly Ser Ala Arg Ser Xaa
1 5

<210> 588
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 588
Ser Gly Arg Ser Xaa
1 5

<210> 589

-278-

<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 589
Ser Gly Arg Ser Ser Xaa
1 5

<210> 590
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 590
Ser Ala Arg Ser Xaa
1 5

<210> 591
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLTATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 591
Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 592
<211> 8

-279-

<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 592
Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 593
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 7
<223> Leucine-therapeutic agent

<400> 593
Arg Gly Ser Ala Arg Ser Xaa
1 5

<210> 594
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 8
<223> Leucine-therapeutic agent

<400> 594
Leu Arg Gly Ser Gly Arg Ser Xaa
1 5

<210> 595
<211> 9
<212> PRT

-280-

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 9

<223> Leucine-therapeutic agent

<400> 595

Leu Arg Gly Ser Gly Arg Ser Ser Xaa
1 5

<210> 596

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Leucine-therapeutic agent

<400> 596

Leu Arg Gly Ser Ala Arg Ser Xaa
1 5

<210> 597

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 8

<223> Alanine-therapeutic agent

<400> 597

Leu Arg Arg Gln Ser Arg Ala Xaa
1 5

<210> 598

<211> 5

<212> PRT

<213> Artificial Sequence

-281-

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is N-Methylsulfonyl-alpha-cyclohexyl-D-Alanine

<221> MOD_RES
<222> 2
<223> Xaa is Abu

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 598
Xaa Xaa Arg Ser Xaa
1 5

<210> 599
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 5
<223> Leucine-therapeutic agent

<400> 599
Arg Ala Arg Ser Xaa
1 5

<210> 600
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa si Alpha-Cyclohexyl-D-alanine

<221> MOD_RES
<222> 2
<223> Abu

<221> MOD_RES
<222> 5

-282-

<223> Leucine-therapeutic agent

<400> 600

Xaa Xaa Arg Ser Xaa
1 5

<210> 601

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is Alpha-Cyclohexyl-D-Alanine

<221> MOD_RES

<222> 2

<223> Abu

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 601

Xaa Xaa Arg Ser Ser Xaa
1 5

<210> 602

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 602

Gln Gly Arg Ser Ser Xaa
1 5

<210> 603

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

-283-

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-D-homophenylalanine

<221> MOD_RES

<222> 2

<223> Xaa is 4Hyp

<221> MOD_RES

<222> 6

<223> Leucine-therapeutic agent

<400> 603

Xaa Xaa Arg Ser Ser Xaa

1

5

<210> 604

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> MOD_RES

<222> 1

<223> Xaa is Methoxycarbonyl-(alpha)-3-methylbenzyl
glutamic acid -delta-methyl ester

<221> MOD_RES

<222> 5

<223> Leucine-therapeutic agent

<400> 604

Xaa Gly Arg Ser Xaa

1

5

<210> 605

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> conjugate

<221> ACETYLATION

<222> 1

<221> MOD_RES

<222> 1

<223> Xaa is D-cyclohexylalanine

<221> MOD_RES

<222> 2

<223> Xaa is 4Hyp

<221> MOD_RES

-284-

<222> 5
<223> Leucine-therapeutic agent

<400> 605
Xaa Xaa Arg Ser Ser Xaa
1 5

<210> 606
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> ACETYLATION
<222> 1

<221> MOD_RES
<222> 1
<223> Xaa is D-Clohexylalanine

<221> MOD_RES
<222> 2
<223> Xaa is Abu

<221> MOD_RES
<222> 6
<223> Leucine-therapeutic agent

<400> 606
Xaa Xaa Arg Ser Ser Xaa
1 5

<210> 607
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-cyanobenzyl))
glutamic acid -delta-methyl ester

<221> AMIDATION
<222> 5

<400> 607
Xaa Gly Arg Ser Leu
1 5

<210> 608
<211> 5
<212> PRT
<213> Artificial Sequence

-285-

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-amidinobenzyl))
glutamic acid -delta-methyl ester

<221> AMIDATION
<222> 5

<400> 608
Xaa Gly Arg Ser Leu
1 5

<210> 609
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> conjugate

<221> MOD_RES
<222> 1
<223> Xaa is Methoxycarbonyl-(alpha-(3-amidinobenzyl))
glutamic acid

<221> AMIDATION
<222> 5

<400> 609
Xaa Gly Arg Ser Leu
1 5

<210> 610
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Conjugate

<221> ACETYLATION
<222> (0)...(0)

<221> MOD_RES
<222> 6
<223> Isoleucine-therapeutic agent

<400> 610
Arg Arg Gln Ser Arg Xaa
1 5

<210> 611
<211> 8
<212> PRT
<213> Artificial Sequence

-286-

<220>

<223> Conjugate

<221> ACETYLTATION

<222> 1

<221> MOD_RES

<222> 8

<223> Isoleucine-therapeutic agent

<400> 611

Leu Arg Arg Gln Ser Arg Ala Xaa

1

5